

DR HSP: Q9Y286; 1075.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR Pfam: PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 3.
KW Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 597
FT
FT
FT DOMAIN 21 483
FT TRANSMEM 484 504
FT DOMAIN 505 597
FT DOMAIN 21 144
FT DOMAIN 145 271
FT DOMAIN 277 360
FT DOMAIN 367 464
FT SITE 565 570
FT SITE 588 593
FT DISULFID 46 106
FT DISULFID 168 301
FT DISULFID 173 233
FT DISULFID 295 344
FT DISULFID 403 448
FT CARBOHYD 142 142
FT CARBOHYD 181 181
FT CARBOHYD 232 232
FT CARBOHYD 292 292
FT CARBOHYD 362 362
FT CARBOHYD 369 369
FT CARBOHYD 387 387
SQ SEQUENCE 597 AA; 65075 MW; 74C13CFA9CDB5BA5 CRC64;
Query Match 33.6%; Score 909; DB 1; Length 597;
Best Local Similarity 41.4%; Pred. No. 1.4e-53;
Matches 212; Conservative 70; Mismatches 164; Indels 66; Gaps 11;
QY 7 LSSLLGGQAMGRFWRVQESVMVPEGLICIVPCSFSPRODWTGSTPAYGYWKAITE 66
Db 139 LSNVNTASDLSRYRLEVPESVTQGLCVSPVCSVLYPHCNVTASSPVYGSWFKEGAD 198
QY 67 TTKGAPVATNHQREVMSTRGRFQLTGDPKNCSLVIRDAQMODSOFYFRVERGSV 126
Db 199 IPCDIPVATNTPSGKVQEDTQGRFLLDGPDQTNCSLSIRDAKGDGSKYVQVREGSR- 257
QY 127 RYFMNDGFLKYALTQKPDVYIPETLFPQGVTVICVFNNAFECPPPPSPFSWTGAALS 186
Db 258 KWNVIYDKLSVHTALTLPFTSIPGTLESQHPNLTCSVPWACEQGTPTTITWNGASTS 317
QY 187 SQGTKSTTSHFSLVSTPRPDHDTDLTCHVDPSRKGVAQRTVRLVAYAPRDLVISIS 246
Db 318 S--LEPTISRSSMLSLIPKPDHGTSLTCQVTLPGAGVTTTRAVRLNISY----- 365
QY 247 RDNTDPPENLRVMVQANRTVLENLNGTSLPVLGQSLCLVCTVTHSSPPARLSWTORG 306
Db 366 -----PPQNLTWTVQGDGTASTTLRNGSALSVLGQSLHLVCAVDNSNPRLSWTWS 419
QY 307 QVLSPQSPDPGVLELPRVOVEHEGFTCHARPLGSHVLSVHYK---KGLISTAF 363
Db 420 LTLSPSQSSLGLVLELPRVHVKEGFTCRAQNPGLSQHLSLSLQNEYTGKMRPISGV 479
QY 364 SNGAFLGIGITALLFLCLALIMKILPKRRTQETPRPRFSRSTILDVINVV---PTAG 420
Db 480 TLGAVGAGATLVLFSLFCILFVVV---RSCRKKSARPAVGVDGTQMETNVRGSAASQ 536
QY 421 FLAQRNQAATNPSRPTLPFGAPSPESKKNQKQYCLPSFPPEPKSTQAPESQEBEL 480
Db 537 FLI-----ESPADSPPHHAPPALATP-----FPE-----EGEI 565
QY 481 HYATLNPFGVPRPPEARMKGTQA---DYAEV 509
Db 566 QYASLSFHKARP---QYPOEQEAGYEVSEI 593

RESULT 12

Q6PJ50 PRELIMINARY; PRT; 468 AA.
ID Q6PJ50
AC Q6PJ50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SIGLEC-like 1.
GN Name=Siglec1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Heltan E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023280; AAH23280.1; -.
DR GO; GO:0004872; F:receptor activity; IDA.
DR GO; GO:0005057; F:receptor signaling protein activity; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 468 AA; 51987 MW; 26A0FF7AD3CA4ACF CRC64;
Query Match 32.4%; Score 878; DB 2; Length 468;
Best Local Similarity 39.0%; Pred. No. 1.4e-51;
Matches 204; Conservative 75; Mismatches 170; Indels 74; Gaps 11;
QY 1 MLLPFLSSLLGGQAMGR-----FWIRVQESVMVPEGLICIVPCSFSPRQ---DWTG 52
Db 1 MLLPFLSSLLGGQAMGR-----FWIRVQESVMVPEGLICIVPCSFSPRQ---DWTG 52
QY 53 STPAYGYWKAITEVTKGAPVATNHQREVMSTRGRFQLTGDPKNCSLVIRDAQMOD 112


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Db 342 QSSATL--SEMMGTFFVSGVATALLFLSVCILLAVRSYRRKPARPAVAVPH----- 392
QY 409 ILDYINVVPTAGLAQKRNQKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKPSST 468
Db 393 --DALKVSVSQNPLVESQADDS-----SEPLESILE 421
QY 469 QAPESQESQELHYATLNFPGVPRPEARMKPGTQADYAEVKF 511
Db 422 AAPSTE--EEHYATLSFHEMKPM-NLWQQDTTTEYSEIKF 461

RESULT 15
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ID AAH23280 PRELIMINARY; PRT; 468 AA.
AC AAH23280;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE SIGLEC-like 1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II;
RC TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer;
RA Strausberg R.
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC023280; AAH23280.1; -. 26A0FF74D3CA4ACF CRC64;
SQ SEQUENCE 468 AA; 51987 MW; 26A0FF74D3CA4ACF CRC64;

Query Match 32.4%; Score 878; DB 2; Length 468;
Best Local Similarity 39.0%; Pred. No. 1.4e-51;
Matches 204; Conservative 75; Mismatches 170; Indels 74; Gaps 11;

QY 1 MLPLLLSLLGGSQMDGR-----FWIRQESVMVPEGLICISVPCSPSYPRQ---DWTG 52
Db 1 MLLLLLLLLLLGKVGQNGQNGFTLNVERKVVQVEGLVLCVPCNFSYLRKRLTDWTD 60
QY 53 STPAYGVFWKAVTETTKGAPVATNQHOSREVEMSTRGRFQITGDPKNGNSLVIRDAQMOD 112
Db 61 SDPVHGFWEYEGTDRRKDSIVATNPIKAVKETRNREFLLGEPWENDCSLNIREIKKD 120
QY 113 ESQYFRVRERGSVYRNFMNDGDFLKVATLTQKPDVYIPETLEPGQPVTVCVFNWAFEE 172
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Db 121 AGLYFFRLERKG-TKYNMMDKMTLVVVTALTNTFQILLPETLEAGHFSNLTCSVPWDCGW 179
QY 173 CPPPSFWTGAALSSQGTKTTSHFSVLSTPSPQDHDLTDLTCHVDFSRKGVSAQRTVRL 232
Db 180 TAPFIFSWTGTSVSFLSTNTTGS--SVLTITPQDQHGTLNLTCCVTLPGTDVSTRMTIRL 237
QY 233 RVAYAPRDLVISISRDNTPOPPENLRVWVSQANRTVLENLNGTSLFVLEGGQSLCLVCVT 292
Db 238 NVSYAPK-----NLTVTIYQGADSVSTILKNGSSLPISGQSRLICST 281
QY 293 HSPPARLSWTQRCQVLSPPSQDPGVLELPRVOVEHEGEFTCHARPLSGSOHVSLSIV 352
Db 282 DSYPPANLWSNDNLTLCPKSLKPGLELFPVHLKHGGVYTCQAQHALGSOHISLSLSP 341
QY 353 HYKGLISTAFSNGAFLGIGITALLFLCLALIMKILPKERTOTE-----TPRPRFSRHS 408
Db 342 QSSATL--SEMMGTFFVSGVATALLFLSVCILLAVRSYRRKPARPAVAVPH----- 392
QY 409 ILDYINVVPTAGLAQKRNQKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKPSST 468
Db 393 --DALKVSVSQNPLVESQADDS-----SEPLESILE 421
QY 469 QAPESQESQELHYATLNFPGVPRPEARMKPGTQADYAEVKF 511
Db 422 AAPSTE--EEHYATLSFHEMKPM-NLWQQDTTTEYSEIKF 461
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Search completed: November 5, 2004, 13:57:39
Job time : 116.542 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 17.3484 Seconds
(without alignments)
1957.231 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLLPILLSLLGGSQMDGR.....RPEARMPKGTDYAEVVKFQ 512

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 56318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/aaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/aaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/aaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/aaa/ECTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	888	32.8	431	3	US-09-038-832-2
2	888	32.8	431	3	US-09-038-832-4
3	831.5	30.7	467	3	US-09-046-736-2
4	800.5	29.6	551	4	US-08-896-537A-2
5	769	28.4	440	3	US-08-759-628-4
6	693.5	25.6	421	3	US-08-759-628-5
7	693	25.6	364	4	US-08-896-537A-3
8	573	21.2	374	3	US-09-046-736-4
9	346	12.8	64	4	US-09-513-999C-7159
10	200	7.4	56	4	US-09-513-999C-4599
11	177.5	6.6	501	2	US-08-408-095-31
12	172.5	6.4	403	4	US-09-638-649-5
13	167	6.2	464	2	US-08-602-725-32
14	155	5.7	321	6	5169835-17
15	153.5	5.7	416	4	US-09-638-649-1
16	153.5	5.7	416	4	US-08-755-235-2
17	152.5	5.6	373	4	US-10-140-002-388
18	151.5	5.6	1241	3	US-09-040-774-2
19	143	5.3	642	1	US-08-617-299-1
20	143	5.3	698	2	US-08-602-725-36
21	143	5.3	734	2	US-08-389-459A-17
22	143	5.3	734	3	US-08-987-867A-17
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24	139.5	5.2	611	3	US-09-707-802-10
25	139.5	5.2	611	3	US-09-591-326-10
26	139	5.1	404	4	US-09-638-649-3
27	138.5	5.1	349	4	US-09-924-103-4
28	138	5.1	354	6	5169835-4
29	136.5	5.0	432	4	US-09-778-510-2
30	136	5.0	1091	3	US-08-986-485-5
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32	135.5	5.0	630	3	US-09-707-802-14
33	135.5	5.0	630	3	US-09-931-326-14
34	134.5	5.0	398	4	US-09-778-510-6
35	134.5	5.0	398	4	US-09-907-794A-84
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37	134.5	5.0	398	4	US-09-902-775A-84
38	134.5	5.0	398	4	US-09-906-700-84
39	134.5	5.0	398	4	US-10-140-002-348
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43	132	4.9	647	5	PCT-US93-00031-23
44	132	4.9	828	1	US-08-261-304-2
45	131.5	4.9	405	4	US-08-755-235-4

ALIGNMENTS

RESULT 1

US-09-038-832-2

; Sequence 2, Application US/09038832

; Patent No. 6146845

; GENERAL INFORMATION:

; APPLICANT: KIKLY, KRISTINE

; APPLICANT: ERICKSON-MILLER, CONNIE

; TITLE OF INVENTION: Sialoadhesin Family Member-2

; TITLE OF INVENTION: (SAF-2)

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/038,832

; FILING DATE: 11-MAR-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/041,886

; FILING DATE: 02-APR-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-50018

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 431 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-038-832-2

Query Match 32.8%; Score 888; DB 3; Length 431;

Best Local Similarity 47.8%; Pred. No. 1.5e-69;

Matches 195; Conservative 52; Mismatches 127; Indels 34; Gaps 6;

1 MLLPLLLSLLGGSCAMDG-----REWIRVQSVMMVEGLCISVPCSFSPYQDWTGST 54
1 MLLPLLLSLLGGSCAMDG-----REWIRVQSVMMVEGLCISVPCSFSPYQDWTGST 60
55 PAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFOLTGDPKAGKNSLVIRDAQMODS 114
61 PVHGWFRAGDRPYQDAPVATNPNPREVQAETQGRFOLLGDIWSNDCSLSIRDARKRDKG 120
115 QYFRVERGSY-----VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
121 SYFRLEGRGSKWSYKQNLVTKQLSVFVLTALTRPDILILGLTSGHSRNLTCVFWA 180
170 FEECPPEFSWGTGAALSQGTPTTSHPSVLSFTPRPDQDHTDLTCHVDFSRKGVSAQRT 229
181 CKQGTTPMISWIGASVSPG--PTTARSSVLTLPKPDQDHTSLTQVTLPGTGVTTTST 238
230 VRLVAVAPRDLVISISRDNTDPPENLRVMMVQANRTVLENLGNSTSLPVLEGQSLCLV 289
239 VRLDVSY-----PPNMLTWTVFGDATASTALNGSSLSVLEGQSLRLV 282
290 CVTHSSPPARLSWTQGVLSQSPQSDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 349
283 CAVNSNPPARLSWTQGVLSQSPQSDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 342
350 LSVHYKKGLISTAFSN--GAFLGIGITALLFL--CLALIIMKILPKR 392
343 LSLQNEGTGSRPVSVQVTLAAVGGAGATATAFLSFCIIIFIIVSCRK 390

RESULT 2

US-09-038-832-4

Sequence 4, Application US/09038832

Patent No. 6146845

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

APPLICANT: ERICKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-2

TITLE OF INVENTION: (SAP-2)

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: RATNER & PRESTIA

STREET: P.O. BOX 980

CITY: VALLEY FORGE

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038,832

FILING DATE: 11-MAR-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/041,886

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX: 846189

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-038-832-4

Query Match

Best Local Similarity 32.8%; Score 888; DB 3; Length 431;

Matches 195; Conservative 52; Mismatches 127; Indels 34; Gaps 6;

QY 1 MLLPLLLSLLGGSCAMDG-----RFWRVQSVMMVEGLCISVPCSFSPYQDWTGST 54

DB 1 MLLPLLLSLLGGSCAMDG-----RFWRVQSVMMVEGLCISVPCSFSPYQDWTGST 60

QY 55 PAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFOLTGDPKAGKNSLVIRDAQMODS 114

DB 61 PVHGWFRAGDRPYQDAPVATNPNPREVQAETQGRFOLLGDIWSNDCSLSIRDARKRDKG 120

QY 115 QYFRVERGSY-----VRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169

DB 121 SYFRLEGRGSKWSYKQNLVTKQLSVFVLTALTRPDILILGLTSGHSRNLTCVFWA 180

QY 170 FEECPPEFSWGTGAALSQGTPTTSHPSVLSFTPRPDQDHTDLTCHVDFSRKGVSAQRT 229

DB 181 CKQGTTPMISWIGASVSPG--PTTARSSVLTLPKPDQDHTSLTQVTLPGTGVTTTST 238

QY 230 VRLVAVAPRDLVISISRDNTDPPENLRVMMVQANRTVLENLGNSTSLPVLEGQSLCLV 289

DB 239 VRLDVSY-----PPNMLTWTVFGDATASTALNGSSLSVLEGQSLRLV 282

QY 290 CVTHSSPPARLSWTQGVLSQSPQSDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 349

DB 283 CAVNSNPPARLSWTQGVLSQSPQSDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLS 342

QY 350 LSVHYKKGLISTAFSN--GAFLGIGITALLFL--CLALIIMKILPKR 392

DB 343 LSLQNEGTGSRPVSVQVTLAAVGGAGATATAFLSFCIIIFIIVSCRK 390

RESULT 3

US-09-046-736-2

Sequence 2, Application US/09046736

Patent No. 6090582

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE

APPLICANT: ERICKSON-MILLER, CONNIE

TITLE OF INVENTION: Sialoadhesin Family Member-3

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980

CITY: Valley Forge

STATE: PA

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/046,736

FILING DATE: 24-MAR-1998

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/041,885

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: Prestia, Paul F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50019

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700

TELEFAX: 610-407-0701

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,574
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0552Q
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 440 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-759-628-4

Query Match 28.4%; Score 769; DB 3; Length 440;
 Best Local Similarity 36.5%; Pred. No. 4.3e-59;
 Matches 190; Conservative 73; Mismatches 163; Indels 94; Gaps 15;

QY 2 LPLLLSLGGQAMGRWIRVQESVMVPEGLCHISVPCSF--SYPRQDWTGSPAYGY 59
 DB 1 MLPLLLPPLWAGALAOERFQEGESLTVQEGLCVLPRLTLP-----ASYVGYGY 55
 QY 60 WFKAVTETTKGA--PVATNHSREVMSRGRFQLAGDPKAGNCSLVIRDAQWQDSQYF 117
 DB 56 WF-----LEGADVATNDPDEVEEETGRPHLLDPKNCSSLIRDARRNNAIF 109
 QY 118 FRVERGSYRVNFMNDGFFLKVTALTKQPDVPIPETLEPG--QPVTVICVFNMAFEECP 175
 DB 110 FRL-KSKMKYGYTSSKIYVRNVALTERENISIP---GPGWPSNLTCSVPWVCEQGT 165
 QY 176 PFSWTCALSSOGTKETTSFHSVLSFTPRPODHDITLCHVDPSKGVSAQRTVRLVA 235
 DB 166 PFSWMSAAPHLLG--PRITQSSVLITP-AQHSNLTCTQVTFPGAGVTMBERTQLNVS 222
 QY 236 YAPRDVLVISRDNTDPDENLWVMSQANRTVLENLNGTSLPVLGGSLCLVVCVTHSS 295
 DB 223 YAPQKVAISI-----FQNSAAFKILQNTSSLVLEGGALRLCDADGN 266
 QY 296 PPARLNTQGVLSFQSDPDGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYK 355
 DB 267 PPAHLSMFQASPPXNATPISNTGVLELPQVGSABEGDFTCRAQHPLGSLQISLSLVHMK 326
 QY 356 K-----GLISTAFSGAFGLGIGTALLFLCLALIIMKILPKRRTOTETPRPRFSRSTIL 410
 DB 327 PEGRAGVGL-----GAVWASITLVFLVCVFEP-----RVKTRKKQPSQCKXT 371
 QY 411 DYINVVPTAGPLAQKNQKATPNRPPLPGAPSPESKKNQKQVQLPSPFEPKSSQA 470
 DB 372 DDVNPVWVSG-----SRGHQFQFGTGVSDHPAEA 401
 QY 471 PESQSOELHYATLNFPGVRPEARMKPGTQADYAEVK 510
 DB 402 GPISDEQELHYAVLHFHKVQPOE-----PKVTDTEYSEIK 437

RESULT 6
 US-08-759-628-5
 Sequence 5, Application US/08759628
 Patent No. 625446
 GENERAL INFORMATION:
 APPLICANT: Altman, Scott W.
 APPLICANT: Rock, Fernando L.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Kastelein, Robert A.
 TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMLIAN PROTEINS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,628
 FILING DATE: 05-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,574
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0552Q
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 421 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-759-628-5

Query Match 25.6%; Score 693.5; DB 3; Length 421;
 Best Local Similarity 43.0%; Pred. No. 1.7e-52;
 Matches 157; Conservative 53; Mismatches 132; Indels 23; Gaps 4;

QY 3 LPLLLSL--GGQAMGRWIRVQESVMVPEGLCHISVPCSFYPRQDWTGSPAYGYWF 61
 DB 1 MPLLLPLLGGSLQEKPVYELQVQKSVTVQEGLCVLPVPCSFYPRWRSWYSSPPLYYWF 60
 QY 62 KAVTETTKGAPVATNHSREVMSRGRFGLTGDPAKGNCSLVIRDAQWQDSQYPERVE 121
 DB 61 RDGEIPYAEVVAIINPDNRVKETQGRFRLDGVQKNCNCSIGDARMEETGSYFPERVE 120
 QY 122 RGSYRVNFMNDGFFLKVTALTKQPDVPIPETLEPG--QPVTVICVFNMAFEECPSPFS 179
 DB 121 RGRDVKYSYQKNLNEVTLIEKPDHLSGPLESGLWRPTRLSCSLPSCVAGPPLTFS 180
 QY 180 WTGAALSSQGTKTTSFHSVLSFTPRQDHDITLCHVDPSKGVSAQRTVRLVAAPR 239
 DB 181 WTGNAXAPMT-PRXAPRELTLTPRDEHGTMLTCOMKQGAQVITEXTVQLNVSTAPQ 239
 QY 240 DLVTSISRDNTDPDENLWVMSQANRTVLENLNGTSLPVLGGSLCLVVCVTHSSPPAR 299
 DB 240 TITIF-----RNGIALEILQNTSYLPVLEGGALRLCDAPSNPPAH 280
 QY 300 LSWTQRCQVLSFQSDPDGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYKGLI 359
 DB 281 LSWFQGSFALNATPISNTGILELRVRSABEGGFTCRAQHPLGFLQIFLNLVSYLPQLL 340
 QY 360 STAPS 364
 DB 341 GPSCS 345

RESULT 7
 US-08-896-537A-3
 Sequence 3, Application US/08896537A
 Patent No. 6590088
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Gentz, Reiner L.

```
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CD33-Like Protein
; FILE REFERENCE: 1488.0480001
; CURRENT APPLICATION NUMBER: US/08/896,537A
; CURRENT FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,481
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-896-537A-3

Query Match      25.6%; Score 693; DB 4; Length 364;
Best Local Similarity 33.2%; Pred. No. 1.5e-52;
Matches 170; Conservative 59; Mismatches 135; Indels 148; Gaps 10;

QY      1 MLLPLLSSLLGGSOAMDGRFIRVOESVMVPEGLCISVPCGSFSPRODWTGSTPAYGYW 60
DB      1 MPELLLLPLWAGALAMPENFLQVESVTVQEGLCVLPCTFFPIPIYDKNSPVHGYW 60
QY      61 PKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESOYFFRV 120
DB      61 FREGAIIISGDSVATNKLQVEQETQGRFLLGSPSRNCSLSIVDARRDNGSYFFRM 120
QY      121 ERSYVRVNFNMDGFLLKVTALTQKPDYVITPTEPGQPVTIVCVFNWAFECPPSPESW 180
DB      121 ERGS-TKYSYKSPQSVSHVTDUTHRPKILIPGTELEPHGSKNLTCSVWACQGGTPPIFSW 179
QY      181 TGAALSSQGTPTTSHFSVLSFTPRPDHDTDLTCHVDPSRKGVSQAQTVRLRAYAPRD 240
DB      180 LSAAPTSLG--PRTHSSVLIITPRPDHGINLTQCVKFAAGVTTERTIQLNVTYVPQ- 236
QY      241 LVISIRONTDPPENLRVMVSOANRTVLENGNCTSLPVLEGQSLCLVCVTHSSPPARL 300
DB      237 ----- 236
QY      301 SWTORGQVLSQSPSDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYKKGLIS 360
DB      237 -----NPTGIFPG-----DGS-----GQET-----RAGLV- 258
QY      361 TAFSGAFIGIGITALLFLCLALIIIMKILPKRRTQTETPRFRFSRHSTILYINVVPTAG 420
DB      259 ----HGAIGAGVATALLALCLIFFIVKTHRRKAARTAVGSDNTHPT----- 302
QY      421 PLAQRNQAQATNSPRTPLPGAPSPESKQKQYQLPSPEPKSSTQAPESQESQEL 480
DB      303 -----TGASPKHQKNSK-----LHGETTSSCSGAAPTVMDEEL 338
QY      481 HYATLNFQVRPRPEARMKPGTQADYAEVKFQ 512
DB      339 HYASLNFHGMNP-----SKDTSTSYSEVRTQ 364

RESULT 8
US-09-046-736-4
; Sequence 4, Application US/09046736
; Patent No. 6030582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-046-736-4

Query Match      21.2%; Score 573; DB 3; Length 374;
Best Local Similarity 29.8%; Pred. No. 5.4e-42;
Matches 156; Conservative 63; Mismatches 138; Indels 166; Gaps 10;

QY      2 LPLPLLSSLLGGSOAMDGR-----FWIRVOESVMVPEGLCISVPCGSFSPRODWTGSTP 55
DB      1 MLLLLLLPLWGRVERVEMQSKNDKSLTMQSSVTVQEGCVHVRCSFSYFVDSQTDSDP 60
QY      56 AYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQ 115
DB      61 VHGYWFRAGNDISWKAPVATNPAWQVESTRDRFLLGDFQTKNCTLSIRDARMSDAGR 120
QY      116 YFRVERGVSVRVNFNMDGFLLKVTALTQKPDYVITPTEPGQPVTIVCVFNWAFECPP 175
DB      121 YFRMEKGN-IKWYKIDQLSVNVTY----- 145
QY      176 PSFSWTGAALSSQGTPTTSHFSVLSFTPRPDHDTDLTCHVDPSRKGVSQAQTVRLRVA 235
DB      146 ----- 145
QY      236 YAPRDLVISIRONTDPPENLRVMVSOANRTVLENGNCTSLPVLEGQSLCLVCVTHSS 295
DB      146 -----PPQNLTVTVFQEGGTASTALGNSSSLSVLEGQSLRLVCAVDN 188
QY      296 PPARLSWTORGQVLSQSPSDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLSVHYK 355
DB      189 PPARLSWTWESLTYPSQSPNPLVLEL-QVHLGDEGEFTCRAQNSLGSQSHVSLNLSLQOE 247
QY      356 -----KGLISTAFSGAFIGITALLFLCLALIIIMKILPKRRTQTETTPRFRSRHS 407
DB      248 YTGKMRPVSGVLL-----GAVGGAGATALVFLSFCVFIWV-----RSCRKKSARP- 293
QY      408 TILDYINVVPTAGTACQKRNQKATNSPRTPLPGAPSPESKKNQKQYQLPSFPPEPKSS 467
DB      294 -----AADVDIGNK-----DANTIRGSASQGNLTESWADDNPRHH 329
QY      468 TQAPESQESQELHYATLNFQVRPRPEARMKPGTQADYAEVK 510
DB      330 GLAAHSSGEEREIQYAPLSPHKGEPO-DLSGQEAATNNEYSEIK 371

RESULT 9
US-09-513-999C-7159
; Sequence 7159, Application US/09513999C
; Patent No. 6783961
```

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.052.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7159
LENGTH: 64
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 28
OTHER INFORMATION: Xaa-His or Gln
US-09-513-999C-7159
Query Match 12.8%; Score 346; DB 4; Length 64;
Best Local Similarity 98.4%; Pred. No. 3.6e-23;
Matches 63; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
131 MNDGFLKVTALTKQPDVPIPETLEPGQPVVICVFNWAFECPPSPSWTGAALSSQGT 190
1 MNDGFLKVTALTKQPDVPIPETLEPGQPVVICVFNWAFECPPSPSWTGAALSSQGT 60
191 KPPT 194
61 KPPT 64
RESULT 10
US-09-513-999C-4599
Sequence 4599, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.052.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 4599
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -16..-1
OTHER INFORMATION: score 11.3
OTHER INFORMATION: seq FLLLSLLGGSSQA/MD
FEATURE:
NAME/KEY: UNSURE
LOCATION: 24
OTHER INFORMATION: Xaa-Ala or Ser
US-09-513-999C-4599
Query Match 7.4%; Score 200; DB 4; Length 56;
Best Local Similarity 89.1%; Pred. No. 1.9e-10;
Matches 41; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
1 MLLPLLSSLLGGSSQAMDGRFWIRVQESVMVPEGLCISVXLLFLP 46

DB 1 MLLPLLSSLLGGSSQAMDGRFWIRVQESVMVPEGLCISVXLLFLP 46
RESULT 11
US-08-408-095-31
Sequence 31, Application US/08408095
Patent No. 5858678
GENERAL INFORMATION:
APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-31
Query Match 6.6%; Score 177.5; DB 2; Length 501;
Best Local Similarity 20.0%; Pred. No. 4.3e-07;
Matches 107; Conservative 82; Mismatches 182; Indels 165; Gaps 24;
QY 25 VQESVMVPEGLCISVFCSP-----SYPRQDWGSTPAYGYWFKAVTETTKGAPVATNHQS 79
DB 80 IQNEMPIREGDVTLSNYSNPSVTRVEW---KPHGAWEEPGLGVLKIQVWMDNTT 135
QY 80 REVEMSTRGRFOLTGDPKNCNCSLVIRDAQMDQESQYFFRVERGSYVRYNFVNDGFLKV 139
DB 136 --TACARCNCSWASPVALNVQYAPRDVVR-----LSWTQRCQVLSPSQ 167
QY 140 TALTKQPDVPIPETLEPGQPVVICVFNWAFECPPSPSW--TGAALSSQGTKPPTSHF 197
DB 168 KPLSE-----IHSNYSVSLQCDPSSSHPK--EVQFPWEXNGRLG---KESQLNF 212
QY 198 SVLSFTPRPDHDTLTCHVDFSRKGVSAQRTVLRVAYAPROLVISISDNTDPDENL 257
DB 213 DSIS---PEDAGS-YSCWYNN--IGQTASKAWTLEVLVAPRLRVSMSPGD----- 258
QY 258 RVMSQANRTVLENLNGTSLPVLEGOCLVGVTHSSPPAR---LSWTQRCQVLSPSQ 313
DB 259 -----QWEGKSATLTCEADNPFVSHYTFWFDNNQ-----SL 291
QY 314 PSDPGVLELPRVQVEHEGETCHARPLGSHQVSL--LSVHYKKGLISTAFNSAGFLGIG 372
DB 292 PHHSQKLRLFPVKVQHSQAYWCQGTNSVKGSRSPSLTLYVYSPETI-----GRVAVG 345
QY 373 ITALLFLCLALIIIMKI---LPXR--RTOTET-----PRFRSRHSTILDYIN 414
DB 346 LGS-----CLAIIILAICGLKQLQRWKTQSQQLQENSSQSQFFVFNKKVRAPLSEGP 401

QY 415 VVPTAGPLAQKQKATPNSRPTLPFGAPSPESK-----KNQKQY 456
Db 402 SLGCYNPMMDGISTYTLTFPEPMNIPRTGDAESSEMQRPRCTDDTVTYSALHKQVGDY 461
QY 457 Q--LPSFPPKSTQAPESQESQELHVAFLNFPVVRPEARMKPGTQADYAEVK 510
Db 462 ENVIDFPB-----DEGHSIELIQFGVERPQAC-----ENVDVILK 500

RESULT 12

US-09-638-649-5
; Sequence 5, Application US/09638649
; Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
; TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5

Query Match 6.4%; Score 172.5; DB 4; Length 403;
Best Local Similarity 23.3%; Pred.No. 8.7e-07;
Matches 101; Conservative 46; Mismatches 139; Indels 147; Gaps 21;
QY 100 NCSLVIRDAQMODESQYFRV--ERGSYVRVNFMDGFLKVTALTQKPDVYIPET-LEP 156
Db 80 NGSLLLPATGIVDEGTFRCRATNRGKVKSNR-----VRVYQIPGKPEIVDPASELTA 134
QY 157 GQPTVY-ICVFNWAECECPSPFSW--TGAALSSQGT-----PTSHSPVLS-F 202
Db 135 SVFNKVGTCVSGSY---PAGTLSWHLPGKLLIPDGKTLVKEETRRHPETGLFTRSEL 191
QY 203 TPRP-QDHDITLCHVDFSRKGSQRTVRLRVAVAPRDLVISISRDNTDPPENLRVMV 261
Db 192 TVIPTQGGTTFESCSFS-LGLPRRRPLNT---APIQL-----RVREPGPPEIGILLV 241
QY 262 SQANRVLNENGNISLFLVLEQSLCLVCVTHSSPPARLSWTQGVLSPSQSPDPGVLE 321
Db 242 BPEGGI-----VAPGTVTLTCAISAQPPQVHHWIKDGAPL-PLAPSP--VIL 286
QY 322 LPRQVHEHEGTEPTCHARHPLGSHVLSLSVHY-----KKGLISTAFSNGA 367
Db 287 LPEVGHADGETYSCVATHSPSHGQPSPPVSIIVTGTGDEGPAEGSVGESGLTALALGI 346
QY 368 FIGITALLFLCLALIMKLLPKRTQETPRPRFRSHSTILDYINVVPTAGPLAQKN 427
Db 347 LGGLGVALL-----VGAIIWEKR 365
QY 428 QKATNSRPTLPFGAPSPESKKNQKQYQLPSPFEPKKSSTOAPESQSEHLYATNLF 487
Db 366 Q-----PREERK-----APESQSEDEE--RAELN- 388
QY 488 FGVRPRPEARMK 500
Db 389 ----QSEAEEMPE 397

RESULT 13

US-08-602-725-32
; Sequence 32, Application US/08602725
; Patent No. 5965710

; GENERAL INFORMATION:
; APPLICANT: BODMER, WALTER F
; APPLICANT: DURBIN, HELGA
; APPLICANT: SNARYN, DAVID
; APPLICANT: STEWART, LORNA MD
; APPLICANT: YOUNG, SUSAN
; APPLICANT: BATES, PAUL A
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,725
; FILING DATE: 02-FEB-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/01816
; FILING DATE: 19-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9317423
; FILING DATE: 21-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 1090-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-602-725-32

Query Match 6.2%; Score 167; DB 2; Length 464;

Best Local Similarity 23.5%; Pred.No. 3.2e-06;
Matches 85; Conservative 52; Mismatches 122; Indels 102; Gaps 18;

QY 5 LLSSLLGGSQAMDGRFVRVQSVVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY 57
Db 19 LLTASLL-----TWNPTTAQLTTESMPFNVAEGKEVLLVHNLPOQ-----LF 63
QY 58 GY-WFKAVTETTKGAPVATHQSRVEMSTRGRFQITGDPAGK-----NCSLIVRDAQ 109
Db 64 GYSWYKG--BRVDG-----NRQIVGAIGTQATPGPANGSGRETIYPNASLLIQNT 113
QY 110 MQBQSQFFRVERGSVYRVNFMNDGFLKVTALTQKPDVYIPETLEPGQPVVICVENWA 169
Db 114 QNDTGFTLVQ-----IKSLVNE-----EATGQPHVY-----141
QY 170 FECPPTPSFWTGAALSSQGTKPTTSHFSYLSFTPRPDHDTLTCHVDFSRKGSQAQT 229
Db 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWNNQSLPVPSP-- 189
QY 230 VRLVAVAPRDL-VISISRDNTDPPENLRVMVSWANET--VLENLNGTSLPVL----- 282
Db 190 -RIQLSNGNATLLSVTRNDTGYECEIQNPVS-ANRSDPVTINVTYGPDTPTSESOT 247
QY 283 ----GQSLCLVCVTHSGSPPARLSWTQGVLSQSPSDPGVLPRVQVHEGEFTCHAR 338

Db 248 YRPGANLSLSCYAASNPAPQYSLWINGTFQOSTQB-----LFIPNITVWNSGSYTCHAN 302

Qy 339 H 339

Db 303 N 303

RESULT 14

Accession No. 5169835-17

Accession No. 5169835

APPLICANT: WAI-YEE, CHAN

TITLE OF INVENTION: PREGNANCY SPECIFIC PROTEINS APEPLICATIONS

NUMBER OF SEQUENCES: 48

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/390,409

FILING DATE: 07-AUG-1989

SEQ ID NO:17:

LENGTH: 321

5169835-17

Query Match 5.7%; Score 155; DB 6; Length 321;
Best Local Similarity 24.3%; Pred. No. 2.2e-05;
Matches 73; Conservative 43; Mismatches 105; Indels 80; Gaps 15;

Qy 58 GY-WFKAIVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPAGK-----NCSLVIRDAQ 109

Db 64 GYSWYKQ--ERVDCNSLIVGY-----VIGTQATPGPAYSGRETIYPNASLLIQNVT 113

Qy 110 MQDESQYFRFRV--ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPET--LEPGQPVTV--ICV 165

Db 114 QNDTGFTTQV-----IKSLDQNE-----EATGQFHYV----- 141

Qy 170 FECCPPPSFSWTGAALSSQTKFTTSHFSVLFTPRPDQHDLDLCHVDPSRKGVSAQRT 229

Db 142 -PELPKPS-----ISSNNSNVEDKDAV-AFTCEPETQDTYLLWVNNQSLPVPSP--- 189

Qy 230 VRLRVAYARDL-VISIRDNTPDPENLRVMVSOANRT--VLENLNGTSLPVLB----- 282

Db 190 -RLQLSNGRNTLLSVTRNDTGPYCEIQNPVS--ANRSDPVLNVYTPDPTTISPST 247

Qy 283 ----GOSLCLVCTHSSPPARLSWQGVLSQSPQSDPGVLELPRVQVHEGEFTCHAR 338

Db 248 YRPGANLSLSCYAASNPAPQYSLWINGTFQOSTQB-----LFIPNITVWNSGSYTCHAN 302

Qy 339 H 339

Db 303 N 303

RESULT 15

US-09-638-649-1

Sequence 1, Application US/09638649

Patent No. 6563015

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Schmidt, Ann Marie

APPLICANT: Yan, Shi Du

TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED

TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 05/95/62175

CURRENT APPLICATION NUMBER: US/09/638,649

CURRENT FILING DATE: 2000-08-14

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn ver. 2.1

SEQ ID NO 1

LENGTH: 416

TYPE: PRT

ORGANISM: Bos Taurus

US-09-638-649-1

Query Match 5.7%; Score 153.5; DB 4; Length 416;

Best Local Similarity 23.5%; Pred. No. 4.2e-05;

Matches 108; Conservative 57; Mismatches 170; Indels 125; Gaps 25;

Qy 62 KAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDP-----AKGNCSLVIRDAQ 109

Db 32 KPLVINCCKGAP-KKPPQOLWKJNT-GRTEAWKVLSPQDQWDSVARVLNGLSLPVG 89

Qy 110 MQDESQYFRFRV--ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPET--LEPGQPVTV--ICV 165

Db 90 IQDEGTFRCRATSRSGKETKSNYR-----VRVQIPGKPEIVDPASELMAGVENKVGTCV 144

Qy 166 FNWAFEECPSPSPSW--TGAALSSQ-----TK--PTTSHF-----SVLSFTPRQDHD 210

Db 145 SEGQY---PAGTLNWLDDGKTLIPDQGVSVKBEETKHPKTKGLTTLHSELNMTPARGG-- 199

Qy 211 TDLTCHVDFS---RKGVSAQRTVRLRVAVAPRDLVISIRDNTPDPENLRVMVSOANRT 267

Db 200 ---ALHETFCSTPTGTPRRALHT---APIQLRVWSEHRCGEGP--NVDAPVLEKQVL 250

Qy 268 VLENLNGTSLPVLGOSLCLVCTHSSPPARLSWQGVLSQSPQSDPG-VLELPRVQ 326

Db 251 VVEPEGGA---VAPGCTVTLTCEAPAPQPPQIHWINDGRPL-----PLPEGPMLLPVEG 302

Qy 327 VEHEGEFTCHARHPLGSHVLSLSVHYK-----GLISTAFSGAFLGIG 372

Db 303 PEDGTYSCVATHPSHGQPSRAVSVTIETGEGTTAGSVGPGLETALTGLGLGLG 362

Qy 373 ITALLFLCLALITMKILPKRTQTETPRPRFSRHSHTILDYINVVPTAGPLAQKRNQKATP 432

Db 363 TVALL-----IGVIMVHRRQ-----RKQBRKVP 387

Qy 433 NSPRTPLPPGAPSPESKKNQKQYQLPSFPE-PKSSTQAP 471

Db 388 E-----NQEEEEERAEINQPEEPEAAESSTGGP 416

Search completed: November 5, 2004, 13:58:21

Job time : 19.3484 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 14.2346 Seconds
(without alignments)
3460.797 Million cell updates/sec

Title: US-09-937-636-3
Perfect score: 2706
Sequence: 1 MLLPILLSLLGSGQAMDCR.....RPEARMPKGTQADYAEVKFQ 512

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	694	25.6	364	2	A30521		myeloid cell surfa
2	528	19.5	403	2	I52590		m33-B isoform - mo
3	304.5	11.3	626	1	A61084		myelin-associated
4	302.5	11.2	620	2	JH0593		Schwann cell myeli
5	295.5	10.9	626	1	BNRT3		myelin-associated
6	289.5	10.7	582	1	BNRT3S		myelin-associated
7	288.5	10.7	637	2	B3785		myelin-associated
8	245	9.1	1694	2	S50065		sioloadhesin - mou
9	227	8.4	862	2	I49583		differentiation an
10	220.5	8.1	868	2	A46512		CD22 homolog/B lym
11	206.5	7.6	647	2	A35648		B-cell adhesion pr
12	202.5	7.5	847	2	JH0371		B-cell adhesion pr
13	186	6.9	526	1	A32164		biliary glycoprote
14	184	6.8	402	2	T03062		probable advanced
15	180	6.7	4391	2	A30896		perlecan precursor
16	167	6.2	321	2	JH0395		biliary glycoprote
17	167	6.2	351	2	JH0396		biliary glycoprote
18	167	6.2	417	2	JH0394		biliary glycoprote
19	167	6.2	464	2	C30127		transmembrane carc
20	156.5	5.8	336	2	C27658		pregnancy-specific
21	155	5.7	3707	2	S18252		heparan sulfate pr
22	153.5	5.7	416	1	A42879		advanced glycosyla
23	151.5	5.6	1241	2	J37190		nephlin - human
24	149	5.5	210	2	JC4122		pregnancy-specific
25	149	5.5	538	2	JC2457		vascular cell adhe
26	148.5	5.5	5175	2	T20992		hypothetical prote
27	148.5	5.5	5198	2	T43290		hemocentin precurs
28	147.5	5.5	1906	1	S68235		myosin-light-chain
29	147	5.4	332	2	JN0067		pregnancy-specific

30	144.5	5.3	26926	1	I38344		titin, cardiac mus
31	143	5.3	702	2	A36319		carcinoembryonic a
32	142.5	5.3	1232	2	T43027		neural cell adhesi
33	141.5	5.2	739	2	JN0581		vascular cell adhe
34	141	5.2	402	2	A54312		pregnancy-specific
35	140.5	5.2	392	1	RWHUPD		poliovirus recepto
36	140.5	5.2	417	1	RWHUPA		poliovirus recepto
37	140.5	5.2	428	2	I57486		pregnancy-specific
38	140.5	5.2	428	2	J50032		pregnancy-specific
39	140	5.2	521	2	S34338		biliary glycoprote
40	140	5.2	628	2	I38000		Lutheran blood gro
41	139.5	5.2	419	2	JC4123		pregnancy-specific
42	139	5.1	404	1	I61596		advanced glycosyla
43	138.5	5.1	349	2	A34815		carcinoembryonic a
44	138.5	5.1	495	2	A55181		pregnancy-specific
45	138	5.1	324	2	G43354		pregnancy-specific

ALIGNMENTS

RESULT 1

A30521
myeloid cell surface antigen CD33 precursor - human
C:Species: Homo sapiens (man)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: A30521
R:Simmons, D.; Seed, B.
J:Immunol 141, 2797-2800, 1988
A:Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid progenit
A:Reference number: A30521; MUID:89009814; PMID:3139786
A:Accession: A30521
A:Molecule type: mRNA
A:Residues: 1-364 <SIM>
A:Cross-references: UNIPROT:P20138
C:Genetics:
A:Gene: GDB:CD33
A:Cross-references: GDB:119762; OMIM:159590
A:Map position: 19q13.3-19q13.4
C:Keywords: glycoprotein; surface antigen; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-259/Domain: extracellular #status predicted <EXT>
F:260-282/Domain: transmembrane #status predicted <TM>
F:283-364/Domain: intracellular #status predicted <CYT>
F:100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 694; DB 2; Length 364;
Best Local Similarity 32.8%; Pred. No. 1e-39;
Matches 168; Conservative 59; Mismatches 137; Indels 148; Gaps 8;

QY	1	MLPILLSLLGSGQAMDCRFRWIRVQESVMPRLCLISVFCSPSYPRQDTGTGTPAYGYW	60
DB	1	MLPILLSLLGSGQAMDCRFRWIRVQESVMPRLCLISVFCSPSYPRQDTGTGTPAYGYW	60
QY	61	FKAVTETTKAPVATNHQSRVEMSTGRFOLTGDPAKNCSLVIRDAQMDSEQYFPRV	120
DB	61	FREGAIISSGSPVATNKLQDEVEETQGRFLLGDPNRNCSLSIVDARRDNGSYFRM	120
QY	121	ERGSYVNFNMDGFFLKVTALTQKPDVYIPETLEPQQPVTVICVFNWAECEPPPSFSW	180
DB	121	ERGSYVNFNMDGFFLKVTALTQKPDVYIPETLEPQQPVTVICVFNWAECEPPPSFSW	180
QY	181	TGALSQGTPTTSHFSLVSTPRPDHDTLTCHVDPSRKGVSQAORTVLRVAVAPRD	240
DB	181	TGALSQGTPTTSHFSLVSTPRPDHDTLTCHVDPSRKGVSQAORTVLRVAVAPRD	240
QY	241	LVAISIRNDTPPPENLRVMSQANVTLENLNGTSLPVLGQSLVCVTHSSPPARL	300
DB	241	LVAISIRNDTPPPENLRVMSQANVTLENLNGTSLPVLGQSLVCVTHSSPPARL	300
QY	238	PTTCGIFP-----GDG-----	247
DB	238	PTTCGIFP-----GDG-----	247
QY	301	SWTORGQVLSPSQSDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLVHYKGLIS	360
DB	301	SWTORGQVLSPSQSDPGVLELPRVQVEHEGEFTCHARHPLGSHVLSLVHYKGLIS	360
QY	248	-----SKQETRAGV-----	258
DB	248	-----SKQETRAGV-----	258


```
QY 242 --VISISRDNTDPPP-----ENLRVMSQA-----NRTVLENL 272
DB 345 GNSVSLQCDFSSSHEKVEQFWEKNGRLLGKESQLNFDISPEDAGSYSCWVNSIGQTA 404
QY 273 GNGTSLPVL-----EGSCLVCVTHSSPPAR-----LSWTQRCQVLSLP 311
DB 405 SKAWTLEVLVAPRRLRVNSPGDQWEGKSATLTCESDANPPVSHYTWFDWNNQ----- 458
QY 312 SOPSPPGVLELPRVQVEHEGEFTCHARHPLGSHQVLSLS-LSVHYKKGLISTAFSNGAFLG 370
DB 459 SLPYHSQKLRLEPVKVQHSYGAWCQGTNSVGKRSPLSTLTIVYSPETI-----GRVA 512
QY 371 IGITALLFLCLALIMKI-----LPRK--RTQETPRPRSRHSTILTDVNVVPTAGPLAQ 424
DB 513 VGLGS-----CLAILLILAICGLQRWRKRTSQOGLQENS-----SGQFF 554
QY 425 KENQKATPNSPTPLPPGAPSPESKKNOKKQVLPSPFPBKSSQAPESQBSQELHYAT 484
DB 555 VNKVKVR-----RAPLSEG-----PHSLGCV-----NPMWEDGISYTT 587
QY 485 LNPFGVRPRPEARMKGTQADYAEVK 510
DB 588 LRF-----PEMNIPRTGDAESSEMQ 607

RESULT 12
JH0371
B-cell adhesion protein CD22 beta splice form precursor - human
N:Alternate names: B-cell membrane protein CD22
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0371; 156171
R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
A:Reference number: JH0371; MUID:91086838; PMID:1985119
A:Accession: JH0371
A:Molecule type: mRNA
A:Residues: 1-847 <WIL>
A:Cross-references: UNIPROT:O60926; GB:X59350; NID:936090; PIDN:CAA42006.1; PID:936091
A:Experimental source: B lymphocyte
A>Note: the authors translated the codon AAT for residue 358 as Met
R:Wilson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A:Reference number: 156171; MUID:93267103; PMID:8496602
A:Accession: 156171
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <WIL2>
A:Cross-references: GB:S61375; NID:9385980; PIDN:AAC18956.1; PID:93184492
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
A:Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IM1>
F:609-661/Domain: immunoglobulin homology <IM2>
F:688-706/Domain: transmembrane #status predicted <TRA>
F:67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 7.5%; Score 202.5; DB 2; Length 847;
Best Local Similarity 21.0%; Pred. No. 5.7e-06;
Matches 98; Conservative 69; Mismatches 182; Indels 117; Gaps 19;

QY 1 MLLPPLLISLLGGSQAMGRCFWI-RVQESVMVPEGLCISVPCFS-----YPRQ 48
DB 3 LLGPWLLLVLLVLAFLSDSSKWFEPETLIYAWEGACVWIPCTYRALDGLDLSFILFHPN 62
```

```
QY 49 DWTGSTPAYWFKAVTETTKGAPVATNHOSREVENMSTRGFQLTGDPKAGNCSLVIRDA 108
DB 63 EYKNNTSKFD--GTRLVYESTKDGKVP-----SEQKRVQFLGDKNK-NCTLSHPV 109
QY 109 QMDESQYFRFRVERGSVRYNFMNDGFFLKVTALTQKPDVVIETLEPGQPVTVICVFN- 167
DB 110 HMDSGQLGRMES-----KTEKMERIHNVSRPPPHIQLPPEIQESQEVTLTCLLNF 165
QY 168 -----WAFEECPPPSFWTGAALSQGTPTTSHFSVLSTFPRPDHDTDLTCHV 217
DB 166 SCGYPIQLQWLLGVBMRQAATVSTSL-----TIKSVFTRSELKFSQWSHHGKIVTCQL 221
QY 218 -DFSRKGVN-----AQRTVRLRVAVAPDLVI-----SISRDNTPPPE--- 255
DB 222 QDADGKFLSNDTVQLNVKHPTKLEIKVTPSDAIVREGDSVTWTCVSSN-----PEYTV 277
QY 256 -----NLR-VMVSOQANR---TVLENLNGTGS----- 277
DB 278 SWLKDGTSLLKQNTFTLNLREVTQDSQKCYCCQVNDVGPGRSEEVFLQVQYAPESPSTVQ 337
QY 278 ---LPVLEGSQLCLVCVTHSSP-PARLSWTQRCQVLSFSPQSPDGVLELRVQVEHEGEF 333
DB 338 ILHSPAVEGSQVEFLCMSLANPLFTNTVYHNGKEM---QGRTEERKWHIPKILPWHAGTY 394
QY 334 TCHARHPLGS--QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALL 377
DB 395 SCVAENILGTGQRGAEILDVQYPPKVTIVIQNPPIREGDVTVL 440

RESULT 13
A32164
biliary glycoprotein 1 precursor, splice form a - human
N:Alternate names: transmembrane carcinoembryonic antigen 1 (TMI-CEA); transmembrane carcinoembryonic antigen 1, splice form b; biliary glycoprotein 1, splice form x
C:Species: Homo sapiens (man)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: A32164; A30127; B30127; A48078; S45663; S65939; A30847; G44476
R:Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I.
Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989
A:Reference number: A32164
A:Contents: erratum
A:Accession: A32164
A:Molecule type: mRNA
A:Residues: 1-526 <HIN>
A:Cross-references: UNIPROT:P13688; GB:J03858; NID:9179439; PIDN:AAA51826.1; PID:9179440
R:Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Hefta, I.
Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A:Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure of biliary glycoprotein I
A:Reference number: A94206; MUID:88320555; PMID:2457922
A:Contents: annotation
A>Note: the sequence shown in this reference has been completely corrected in reference 1
R:Barnett, T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J.; Ke J. Cell Biol. 108, 267-276, 1989
A:Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs
A:Reference number: A92752; MUID:89139550; PMID:2537311
A:Accession: A30127
A:Molecule type: mRNA
A:Residues: 1-526 <BAR1>
A:Cross-references: EMBL:X16354; NID:937197; PIDN:CAA34404.1; PID:937198; EMBL:X14784
A:Experimental source: splice form a
A:Accession: B30127
A:Molecule type: mRNA
A:Residues: 1-319, 'D', 417-526 <BAR2>
A:Cross-references: EMBL:X14831; NID:937199; PIDN:CAA32940.1; PID:937200; EMBL:X14784
A:Experimental source: splice form b
R:Barnett, T.R.; Drake, L.; Pickle II, W.
Mol. Cell. Biol. 13, 1273-1282, 1993
A:Title: Human biliary glycoprotein gene: characterization of a family of novel alternative splicing variants
A:Reference number: A48078; MUID:93140765; PMID:8423792
A:Accession: A48078
A:Molecule type: mRNA
A:Residues: 124-141, 'H', 417-526 <BAR3>
A:Cross-references: GB:M76742; NID:9179480; PIDN:AAA57142.1; PID:9179481
```


Experimental source: splice form x

Note: sequence extracted from NCBI backbone (NCBIN:123602, NCBI:123606)

Note: neither the complete nucleic acid sequence nor the complete translation are shown

Huback, W.; Nedellec, P.; Turbide, C.; Stammers, C.P.; Barnett, T.R.; Beauchemin, N.

J. Biochem. 223, 529-541, 1994

Title: Transcriptional control of the human biliary glycoprotein gene, a CEA gene family

Accession number: S45664; MUID:94333343; PMID:8055923

Accession: S45664

Status: preliminary

Molecule type: DNA

Residues: 1-21 <H>

Cross-references: EMBL:X67277; NID:929447; PIDN:CAA47694.1; PID:g606777

Nedellec, P.; Turbide, C.; Beauchemin, N.

J. Biochem. 231, 104-114, 1995

Title: Characterization and transcriptional activity of the mouse biliary glycoprotein

Accession number: S65939; MUID:95354678; PMID:7628460

Accession: S65939

Status: preliminary; translation not shown

Molecule type: DNA

Residues: 1-21 <NED>

Cross-references: EMBL:X67277; NID:929447; PIDN:CAA47694.1; PID:g606777

Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992

Note: only a part of the coding sequence is given

Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstrom, S.

Genomics 14, 384-390, 1992

Title: Identification of three new genes and estimation of the size of the carcinoembryonic antigen precursor gene

Accession number: A44476; MUID:93052339; PMID:1427854

Contents: annotation; alignment of related sequences

Genetics:

Gene: GDB:BCP

Cross-references: GDB:127992; OMIM:109770

Map position: 19q13.2-19q13.2

Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein

F1-136/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>

F1-34/Domain: signal sequence #status predicted <SIG>

F35-526/Product: biliary glycoprotein 1, splice form a #status predicted <MATA>

F35-428/Domain: extracellular #status predicted <EXT>

F35-319, '417-526/Product: biliary glycoprotein 1, splice form b #status predicted <M>

F35-319, '417-526/Product: biliary glycoprotein 1, splice form x #status predicted <M>

F160-217/Domain: immunoglobulin homology <IMM1>

F252-301/Domain: immunoglobulin homology <IMM2>

F341-398/Domain: immunoglobulin homology <IMM3>

F425-454/Domain: transmembrane #status predicted <TM>

F453-526/Domain: intracellular #status predicted <INT>

F104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/B1

Query Match 6.9%; Score 186; DB 1; Length 526;

Best Local Similarity 21.5%; Pred. No. 4.2e-05;

Matches 130; Conservative 80; Mismatches 200; Indels 196; Gaps 31;

QY 5 LLLSSLLGSGQMDGFWVQESVWVPEGLCISVP-----CSFSYPRDWTGSTAY 57

DB 19 LUTASLL-----TFWAPPTTAQTTFSPNVAEGVLLVHNUPOQ-----LF 63

QY 58 GY-WPKAVTETTKGAPVATNHSREVMSTGRFQLTGDFPAK-----NCSLVIRDAQ 109

DB 64 GYSWYKG--ERVDS-----NRQIVGVAIGTQATPGPANSGRETIYVNASLLIQNTV 113

QY 110 MQDESQYFRVERGVSRYVFNMDGFLKVTALTQKPDVYIPETLEPQPVTVICVFWNA 169

DB 114 QNDTGTITLQV-----IKSLDVAE-----EATQGHVY----- 141

QY 170 FEECPSPSWTGAALSSQGTPTTSHFSLGFTPRPDQDHTDLTCHVDFSGKVSQAQT 229

DB 142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWVNNQSLPSP--- 189

QY 230 VRLRVAYAPDL-VISISRDNDPDPENLRVWVSQAQNT--VLENLNGTSLFVLE----- 282

DB 190 -RLQSLNGNRITLLSVTNDTGPVECEIQNPVS--ANRSDPVTLVNTVGPDTPTTSPSDT 247

QY 283 ----GOSLCLVCTHSSPEARLSWTQGVLSQPSQPSDGVLELPRVQVHEGFTCHAR 338

Db 248 YVRGANLSVCAASNPAAQYSMLNGTFOQSTOE-----LFIPNITVNNSGSYTCAN 302

QY 339 HPL-GSQHVSLSLHYKKGILSTAFS-----NCAFLIGITALLFLCLA 382

Db 303 NSVTGCRNTTV-----KTIIVTSLSPVAAKPGIKASKTIVTGDKDSVNL-----CST 350

QY 383 L---IIMKILPKRRTQTETPRPFRSHSTILDYINVP-----TAGP 421

Db 351 NDTGISIRWFFKQSLPSSSEMKLSQGNLTLS--INPVKREDAGTYWCEVFNPKNSQSDP 409

QY 422 LAQRKNQKATNSPRTPLPPCA-----PSPESKKN 451

Db 410 IMLNVNVALFQ--ENGLSPGAIAGIVGVVALVALLAVALACFLHFGKTRASDQDLT 467

QY 452 QKKVQLPSPFPKPSSTQ--APESQESQELHYATLNFPGVVRP-RPEARMPK--GTQADY 506

Db 468 EHK-----PSVSNHTQDHSNDPKNKNEVYSLNFEAQQTPTQSASPSLTATLIY 520

QY 507 AEVKPQ 512

Db 521 SEVKKQ 526

RESULT 14

T09062

probable advanced glycosylation end-products receptor precursor - mouse

N:Alternate names: RAGE

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09062

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Set

submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region

A:Reference number: Z16543

A:Accession: T09062

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-402 <ROW>

A:Cross-references: UNIPROT:O35444; EMBL:AF030001; NID:g2564945; PID:g2564950

C:Genetics:

A:Gene: RAGE

A:Map position: 17

A:Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1; 272/3; 320/1; 329/1; 371/2

C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology

C:Keywords: receptor; transmembrane protein

F:31-100/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 184; DB 2; Length 402;

Best Local Similarity 23.4%; Pred. No. 4.1e-05;

Matches 101; Conservative 46; Mismatches 139; Indels 146; Gaps 20;

QY 100 NCSLVIRDAQMQDESQYFFRV--ERGSYVRYNMDGFFLKVTALTQKPDVYIPET-LEP 156

Db 80 NGSLLLPATGIVDEGTFRCATNRKGEKVSRYR-----VRVYQIPGKPIVDPASLTA 134

QY 157 GQPVTV-ICVFNWAFECPPPSFSW--TGAALSSQGTK-----PTTSFVSLS-F 202

Db 135 SVPNKVTCTVSEGSY---PAGTILSHLDGKLLIPDGKETLVKESTRRHPTGLFLRSEL 191

QY 203 TPRQDHTDITLCHVDFSRKGVSAQTRVLRVAYAPDLVISISRDNDPDPENLRMVVS 262

Db 192 TVIPTQGTHTFTSCFS-LGLPERRPLNT---APIQL-----RVREPGPPGIGLLVE 241

QY 263 QANRTVLENLNGTSLPVLEGOSLCLVCVTHSSHPPARLSWTQGVLSQPSQSDPGVLEL 322

Db 242 PEGGI-----VAPGGTVITLCAISAGPPQVHWIKDCAPI-PLASFP--VLLL 286

QY 323 PRVQVEHEGFTCHARPLGSHQVLSLSVHY-----KKGLISTAFSNGAF 368

Db 287 PEVGEDEGTYSVATHPSHGPQESPPVSTRVTETGDEGPAEGSGVSGSLGTALALGIL 346

QY 369 LGICITALLFLCLALLIMKILPKRRTQTETPRPFRSHSTILDYINVPVTPAGLAKRNQ 428

Db 347 GGLGVALL-----VCAILLRKEQ 365

QY 429 KATPNSRTPLPAGAPSPKXKQKQVQLPSPFPGKSTQAPESQESQELHYATLNPP 488
|||||:|||||
Db 366 -----PRRERK-----APESQDEEE--RAELN-- 387

QY 489 GVRPRPEARMK 500
|||||:|||||
Db 388 ----QSEAEWPE 396

RESULT 15

A38096

N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote
C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 12-Jul-2004

A;Accession: A38096; S19256; S79946; A1059; A40306; B33625; A41736

R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.

J. Biol. Chem. 267, 8544-8557, 1992

A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membr
tor, laminin, neural cell adhesion molecules, and epidermal growth factor.

A;Reference number: A38096; MUID:92235084; PMID:1569102

A;Accession: A38096

A;Molecule type: mRNA

A;Residues: 1-4391 <MUR>

A;Cross-references: UNIPROT:P98160; GB:M85289; NID:G184426; PIDN:AAA52700.1; PID:G184427

R;Kallunki, P.; Tryggvason, K.

J. Cell Biol. 116, 559-574, 1992

A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro
ell adhesion molecules, and epidermal growth factor.

A;Reference number: A41736; MUID:92112994; PMID:1730768

A;Accession: S19256

A;Molecule type: mRNA

A;Residues: 1-57, D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R',
71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3

A;Cross-references: EMBL:X62515; NID:G23469; PIDN:CAA4373.1; PID:G29470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.

Genomics 10, 389-396, 1991

A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g
submitted to the EMBL Data Library, October 1991

A;Reference number: S77946

A;Accession: S77946

A;Molecule type: mRNA

A;Residues: 1-57, D', 59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R',
71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-4

A;Cross-references: EMBL:X62515; NID:G23469; PIDN:CAA4373.1; PID:G29470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.

Genomics 10, 673-680, 1991

A;Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellula
A;Reference number: A40306; MUID:91365376; PMID:1679749

A;Accession: A40306

A;Molecule type: mRNA

A;Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 <DOD>

A;Cross-references: GB:M64283; NID:G184424; PIDN:AAA52699.1; PID:G184425

R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den
J. Cell Biol. 105, 3199-3211, 1989

A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal
anes.

A;Reference number: A33625; MUID:90078352; PMID:2687294

A;Accession: B33625

A;Molecule type: protein

A;Residues: 1379-1384, 'X', 1386-1398, 'X', 1390-1398 <HE2>

A;Accession: A33625

A;Molecule type: protein

A;Residues: 2166-2171, 'X', 2173-2175, 'X', 2177-2185 <HE3>

A;Note: peptide potentially matches four different regions of sequence shown

C;Genetics:

A;Gene: GDB:HSPG2

A;Cross-references: GDB:126372; OMIM:142461

A;Map position: lp36.1-1p36.1

C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembrar

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-4391/Product: perlecan #status predicted <MAT>

F;22-193/Domain: I <DOM1>

F;194-530/Domain: II <DOM2>

F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>

F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>

F;531-1676/Domain: III <DOM3>

F;1159-1206/Domain: laminin-type EGF-like homology <LEG>

F;1583-1610/Domain: laminin-type EGF-like homology <EG7>

F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>

F;1677-3686/Domain: IV <DOM4>

F;2007-2034/Domain: transmembrane #status predicted <TRM>

F;3687-4391/Domain: V <DOM5>

F;3845-3880/Domain: EGF homology <EGF1>

F;3888-3921/Domain: EGF homology <EGF>

F;3993-4106/Domain: laminin G repeat homology <LG2>

F;4147-4175/Domain: EGF homology <EGF2>

F;4149-4151/Region: motor neuron attachment (L-R-E) motif

F;4299-4301/Region: motor neuron attachment (L-R-E) motif

F;65.71.76/Binding site: heparan sulfate (Ser) (covalent) #status predicted

F;89.554.1755.2121.3072.3105.3279.3780.3836.4068/Binding site: carbohydrate (Asn) (coval

F;2995.9333.4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 6.7%; Score 180; DB 2; Length 4391;

Best Local Similarity 20.4%; Pred. No. 0.0015;

Matches 129; Conservative 68; Mismatches 214; Indels 222; Gaps 30;

QY 18 DGRWIRVOESVMVPEGLICTSVPCSFSPQRD--WT--GSTPA-----XYW----- 60

Db 3119 EGPVWVKGVATLE--CVSA-----GEPRSSARWTRISSTPAKLEORTVGLMDSHAVLQ 3171

QY 61 -----FKAVTTTKGAPVATNHSQREVMSVTRG----- 88

Db 3172 ISSAKPSDAGTYVCLQNALGTAQKQVEVIVDTGAMAFAPQVQAEEALTVEAGHTATL 3231

QY 89 RFQJTGTPA-----KGNCSLVIRDAQMCDESQYFRVERGVSYYNF 130

Db 3232 RCSATGSPAPTHWSKURSLPWOHRLEGDTLLIPRVAQ--QDSQYI-----CNA 3280

QY 131 MNDGFFLKVTAAL--TQKPD--VIYFE--TLEPGQVTVICVFNWAFEECPSPSFTGAA 184

Db 3281 TSPAGHAEATILLHVESPPYATTVPEHASVQAGETVOLQCLAHGT----PLTTFQWSRVG 3336

QY 195 LSSQGTRETTSHFSVLSFTPRPDHDTDLCHVDYFSKGVSAQRTVLRVAYAPRDL--VI 243

Db 3337 SSLFGR--ATARNELLHFERAAPDSGRYCRV--TNKVGSAEAFQALLVQGPFGSLPAT 3392

QY 244 SISRDNTDPPENLRVMVQSANRVLENLNGTSLPVL-----QQSLCLVCVTHSSPPAR 299

Db 3393 SIPAGSRP-----TVQVT-----PQLETKSIGASVEFFHCAPVSDQGTQ 3430

QY 300 LSWTQRCQVLSPSQSPFGVLELPRVQVEHEGETCHARPLGSHVLSLSLVHYKGLI 359

Db 3431 LRWFKEGQLPFGHSVDGVLRILQNLQSCQGTVICOAHGFWGKAQASQALVIOALPSVL 3490

QY 360 STAFSNGAFLGIGTALLFLCLALIIMKILPKRTQTETPREFS----- 404

Db 3491 INIRTSVQTVVVG--HAVEFECLAL-----GDPKQVTSKVGHLRPGIVQS 3536

QY 405 -----RHSTILD-----YINVVPTAGP-----LAQKRNQKATPNSRTP----- 438

Db 3537 GGVVRIAHVELADAGQYKCTATNAAGTTQSHVLLLVQALPOISMPEQVVRVPAAGSAVPPC 3596

QY 439 LPFGAPSPESKKNQKQVQLPSFPKPSSTQAPESQESQELHYATLNFPGRPR----- 493

Db 3597 IASGYPTPDISWS-KLDGSLP-----PDSR-----LENNMLPSPVRPDAGTY 3639

Ox 494 -----PEARMPKGTQADYA 507
3640 VCTATNRQGVKAFALQVPERVVVFYFTQTFYS 3672

Search completed: November 5, 2004, 13:51:01
Job time : 18.2346 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 59.6073 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-3

Perfect score: 2706

Sequence: 1 MLPLLLSLGGSQAMDR.....RPEARMPKGTQDYAEVKFQ 512

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2706	100.0	512	3 AAY97542	Aay97542 Human obe
2	2580.5	95.4	697	5 AAU87087	Aau87087 Sialic ac
3	2576.5	95.2	697	6 ADA27153	Ada27153 Human nov
4	2576.5	95.2	697	7 ADD26582	Add26582 Siglec-10
5	2576.5	95.2	697	8 ADI37010	Adi37010 Novel hum
6	2576.5	95.2	697	8 ADL82805	Adl82805 Human PRO
7	2417	89.3	710	7 ADD19314	Add19314 Human sec
8	2278	84.2	544	5 AAU87074	Aau87074 Sialic ac
9	2265	83.7	544	2 AAY41724	Aay41724 Human PRO
10	2265	83.7	544	3 AAB44280	Aab44280 Human PRO
11	2265	83.7	544	4 AAU29082	Aau29082 Human PRO
12	2265	83.7	544	6 ABUS8458	Abus8458 Human PRO
13	2265	83.7	544	6 ABUS8006	Abus8006 Novel hum
14	2265	83.7	544	6 ABUS4321	Abus4321 Human sec
15	2265	83.7	544	6 ABR66195	Abr66195 Human sec
16	2265	83.7	544	6 ABR65585	Abr65585 Human sec
17	2265	83.7	544	6 ABUS9525	Abus9525 Human sec
18	2265	83.7	544	6 ABUS2764	Abus2764 Human PRO
19	2265	83.7	544	6 ABR89895	Abr89895 Novel hum
20	2265	83.7	544	6 ABR68134	Abr68134 Human sec
21	2265	83.7	544	6 ABUS96187	Abus96187 Novel hum
22	2265	83.7	544	6 ABUS2618	Abus2618 Human sec
23	2265	83.7	544	6 ABO08695	Abo08695 Human sec
24	2265	83.7	544	6 ABO02747	Abo02747 Human sec
25	2265	83.7	544	6 ABR74901	Abr74901 Human sec

ALIGNMENTS

RESULT 1

AA97542

ID AAY97542 standard; protein; 512 AA.

XX

AC AAY97542;

DT 12-FEB-2001 (first entry)

DE

Human obesity protein binding protein-2 homologue #1.

XX

Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;

obesity-related disorder; therapy.

KW

Homo sapiens.

OS

WO200059942-A2.

XX

12-OCT-2000.

XX

22-MAR-2000; 2000WO-US006682.

XX

02-APR-1999; 99US-0127667P.

XX

(ELIL) LILLY & CO ELI.

PA

Su EW, Wei J;

XX

WPI: 2000-664992/64.

DR

N-PSDB; AAA37847.

DR

New human obesity protein binding protein-2 homologue nucleic acids,

polynucleotides and polypeptides useful for producing medicament for

treating obesity and/or obesity-related disorders.

XX

Claim 9; Page 86-88; 92pp; English.

XX

This sequence is a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro.

Antigenic epitope-bearing peptides and polypeptides are useful for

raising or screening antibodies that specifically binds to the hOB-BP2h

CC

polypeptides

```

XX      Sequence 512 AA;
30
XX      Query Match.
XX      Best Local Similarity 100.0%; Score 2706; DB 3; Length 512;
XX      Matches 512; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
DB      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
QY      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQDGLTCDPAKGNCSLVIRDAQVQDSQYFFRV 120
DB      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQDGLTCDPAKGNCSLVIRDAQVQDSQYFFRV 120
QY      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
DB      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
QY      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
DB      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
QY      241 LVISISRDNTPDPEENLRVMVSOANRTVLENLNGTSLPVLEGQSCLVCVTHSSPPARL 300
DB      241 LVISISRDNTPDPEENLRVMVSOANRTVLENLNGTSLPVLEGQSCLVCVTHSSPPARL 300
QY      301 SWTQRGVLSPSQSPDGVLELPRVQVHEGEGFTCHARHPLGSHQVLSLSVHYKKGLIS 360
DB      301 SWTQRGVLSPSQSPDGVLELPRVQVHEGEGFTCHARHPLGSHQVLSLSVHYKKGLIS 360
QY      361 TAFSNGAFLGIGITALLFICLAIINKILPKRRTQTTETPRPFRSHSTILDYINVVPTAG 420
DB      361 TAFSNGAFLGIGITALLFICLAIINKILPKRRTQTTETPRPFRSHSTILDYINVVPTAG 420
QY      421 PLAQRNCKATPNSPTLPPGAPSPESKKNQKQYQLPSFPPEKSSSTQAPESQSQEEL 480
DB      421 PLAQRNCKATPNSPTLPPGAPSPESKKNQKQYQLPSFPPEKSSSTQAPESQSQEEL 480
QY      481 HYATLNPFGVRPRPEARMKGTQADYAEVKFQ 512
DB      481 HYATLNPFGVRPRPEARMKGTQADYAEVKFQ 512
RESULT 2
ID      AAU87087
AC      AAU87087 standard; protein; 697 AA.
AC      AAU87087;
DT      05-JUN-2002 (first entry)
XX      Sialic acid-binding Ig-related lectin, Siglec-BMS-I3-995-3.
DE      Human, sialic acid-binding Ig-related lectin; SIGLEC; asthma;
KW      immune system disease; leukaemia; allergy; inflammatory disease;
KW      tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
KW      psoriasis; rheumatoid arthritis; conjunctivitis.
XX      Homo sapiens.
OS      Synthetic.
XX      WO200208257-A2.
XX      31-JAN-2002.
XX      20-JUL-2001; 2001WO-US023082.
XX      21-JUL-2000; 2000US-0220139P.
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX      Longphre M, Chang H, Whitney G;

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XX      WPI: 2002-241565/29.
DR      N-PSDB; ABK43373.
XX      Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
PT      molecules useful for treating immune system diseases such as asthma,
PT      leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX      Example 11; Fig 6; 209pp; English.
XX      The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
CC      related lectin) protein (I). Pharmaceutical compositions comprising (I)
CC      are useful for treating immune system diseases such as asthma, leukaemia
CC      or other allergic or inflammatory diseases. Extracellular domains of (I)
CC      represent potential markers for screening, diagnosis, prognosis, follow-
CC      up assays, and imaging methods. (I) is useful as a target for drugs which
CC      inhibit inflammation, tissue damage and remodeling in asthma, and
CC      inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
CC      disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
CC      also useful for monitoring the course of disease or disorders, and for
CC      identifying agents that bind with and/or modulate the biological activity
CC      of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
CC      useful in diagnosis and/or prognosis methods, and to detect the presence
CC      and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
CC      proteins in a biological sample. (II) are useful as nucleic acid probes
CC      are useful for screening genomic library to isolate a genomic clone of
CC      SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
CC      diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
CC      The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
CC      expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
CC      AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
CC      invention.
XX      SQ      Sequence 697 AA;

```

```

Query Match      95.4%; Score 2580.5; DB 5; Length 697;
Best Local Similarity 73.2%; Pred. No. 3.6e-195;
Matches 510; Conservative 1; Mismatches 1; Indels 185; Gaps 2;
QY      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
DB      1 MLLPLLSSLLGGQAMDGFWIRVQESVMVPEGLCISVPCSFSPYRQDWTGSTPAYGW 60
QY      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQDGLTCDPAKGNCSLVIRDAQVQDSQYFFRV 120
DB      61 FKAVTETTKGAPVATNHQSRVEMSTGRFQDGLTCDPAKGNCSLVIRDAQVQDSQYFFRV 120
QY      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
DB      121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFECPPPSFSW 180
QY      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
DB      181 TGAALSSQGTGKPTTSHFSVLSFTPRQDHDLDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
QY      241 LVISISRDNTPD-----
DB      241 LVISISRDNTPD-----
QY      253 -----PPENLRVMVSOANRTVLE 270
DB      301 WGRPLGLGLFVGKAGDSGRYTCRAENRLGSGQRALDLSVQYPPENLRVMVSOANRTVLE 360
QY      271 NLNGTSLPVLEGQSCLVCVTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 330
DB      361 NLNGTSLPVLEGQSCLVCVTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 420
QY      331 GEFTCHARHPLGSHQVLSLSVHY-----
DB      421 GEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGJHCSCSSQASPAPSLRWMLGE 480
QY      355 -----K 355

```

Db 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGGLSSGLRLRCBANNVHGAGQSGSILQLPDK 540
 QY 356 KGLISTAFNGAFGLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 415
 Db 541 KGLISTAFNGAFGLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 600
 QY 416 VPTAGLAKRCKATPNSRPTPLPGAPSPSKNKKOYOLPSPPEPKSSTQAPESQE 475
 Db 601 VPTAGLAKRCKATPNSRPTPLPGAPSPSKNKKOYOLPSPPEPKSSTQAPESQE 660
 QY 476 SOELHYATLNFPGVPRPEARMKPKTQADYAEVKFQ 512
 Db 661 SOELHYATLNFPGVPRPEARMKPKTQADYAEVKFQ 697

RESULT 3
 ADA27153
 ID ADA27153 standard; protein; 697 AA.
 XX
 AC ADA27153;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human novel secreted protein from cDNA HDPCL05 #2.
 XX
 KW cytostatic; antiinflammatory; immunomodulator; neuroprotective;
 KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KW neurological disorder; blood clotting disorder; food additive;
 KW preservative; human; secreted protein.
 XX
 OS Homo sapiens.
 XX
 PN US2003055231-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 29-OCT-2001; 2001US-00984130.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99MO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.
 XX
 PA (NIJU/) NI J.
 PA (YOUN/) YOUNG P E.
 PA (KENN/) KENNY J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIY/) WEI Y.
 PA (GREE/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 PA (LIUD/) LIU D.
 PA (CROC/) CROCKER P R.
 XX
 PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM, Liu D, Crocker PR;
 XX
 DR WPI: 2003-567103/53.
 DR N-PSDB; ADA27152.
 XX
 PT New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 XX
 PS Claim 11; Page 383-385; 454pp; English.
 XX
 CC The invention relates to an isolated nucleic molecule that is at least
 CC 98% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC defined in the specification, its species homologue, a variant or allelic

CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridising under conditions the polynucleotide, where the polynucleotide
 CC does not hybridise under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide), the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity
 CC in a biological assay and identifying the protein in the supernatant
 CC having the activity). The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation and other immune
 CC disorders, neurological and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.
 XX
 SQ Sequence 697 AA;

Query Match 95.2%; Score 2576.5; DB 6; Length 697;
 Best Local Similarity 73.0%; Pred. No. 7.4e-195;
 Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

QY 1 MLLPLLSSLLGGSCAMDGRFWIRVQESVMVPEGLCISVPCSFYSPRODWTGSPAYGYW 60
 Db 1 MLLPLLSSLLGGSCAMDGRFWIRVQESVMVPEGLCISVPCSFYSPRODWTGSPAYGYW 60
 QY 61 FKAVTETTKGAPVATNHQSREVENSTRGRFOLTGDPAKGNCSLVIRDAQMDESOYFRRV 120
 Db 61 FKAVTETTKGAPVATNHQSREVENSTRGRFOLTGDPAKGNCSLVIRDAQMDESOYFRRV 120
 QY 121 ERGSYRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQVTVICVFNWAFEECPSPFSW 180
 Db 121 ERGSYRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQVTVICVFNWAFEECPSPFSW 180
 QY 181 TGAALSSQGTPTTSHSFVLSFTPRPDHDTDLTCHVDTSRKGVSQRTVRLRYAYAPRD 240
 Db 181 TGAALSSQGTPTTSHSFVLSFTPRPDHDTDLTCHVDTSRKGVSQRTVRLRYAYAPRD 240
 QY 241 LVISISRDNTPD----- 252
 Db 241 LVISISRDNTPALBPQGNVPYLEAQKQFLRLCAADSPATLSWVLQNRVLSSSH 300
 QY 253 -----PENLRVMVSOANRTVLE 270
 Db 301 WGRPLGLELPGVKAGDSGRYTCBAENRLGQQRAIDLSVOYPPENLRVMVSOANRTVLE 360
 QY 271 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTORGVLSPSQSDPGVLELPRVQVEHE 330
 Db 361 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTORGVLSPSQSDPGVLELPRVQVEHE 420
 QY 331 GEFTCHARHPLGSHVLSLSLVHY----- 354
 Db 421 GEFTCHARHPLGSHVLSLSLVHYSPKLLGPSCSWEAEGLHCSCSSQSPAPFSLRWMLGE 480
 QY 355 -----K 355
 Db 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGGLSSGLRLRCBANNVHGAGQSGSILQLPDK 540
 QY 356 KGLISTAFNGAFGLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 415

541 KGLISTAFSNGAFGLIGITALLFLCLALIMKILPKRRTQTETPRFRSHSTILDYINV 600
 416 VPTAGPLAQRNKAATNSPTPLPGAPSPESKKNQKQYQLPSPFPKSSTOAPESQ 475
 601 VPTAGPLAQRNKAATNSPTPLPGAPSPESKKNQKQYQLPSPFPKSSTOAPESQ 660
 476 SQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 512
 661 SQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 697

RESULT 4

ADD26582

ID ADD26582 standard; protein; 697 AA.

XX AC ADD26582;

XX 15-JAN-2004 (first entry)

XX Siglec-10 amino acid sequence SEQ ID NO:7.

XX human; cell surface protein; immunoglobulin; BGS-19; cytostatic;
 XX gynaecological; immunosuppressive; antiinflammatory; antiasthmatic;
 XX antidiabetic; dermatological; gene therapy.

XX Homo sapiens.

XX W02003083078-A2.

XX 09-OCT-2003.

XX 28-MAR-2003; 2003WO-US009676.

XX 28-MAR-2002; 2002US-0368422P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Lee LM, Feder JN, Siemers NQ, Wu S, Chen J;

XX WPI; 2003-804052/75.

XX New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful
 XX for preventing, treating or ameliorating a medical condition, such as a
 XX disorder related to aberrant immunoglobulin cell surface receptor
 XX activity.

XX Example 1; SEQ ID NO 7; 224pp; English.

XX The present invention describes human cell surface protein with
 XX immunoglobulin folds, designated BGS-19 (I). (I) has cytostatic,
 XX gynaecological, immunosuppressive, antiinflammatory, antiasthmatic,
 XX antidiabetic and dermatological activities, and can be used in gene
 XX therapy. (I) can be used for preventing, treating or ameliorating a
 XX medical condition, such as a disorder related to aberrant immunoglobulin
 XX cell surface receptor activity; a cellular adhesion disorder; a disorder
 XX related to hyper- or hypo-immunoglobulin receptor activity; a disorder
 XX related to aberrant signal transduction; a reproductive disorder; a
 XX female reproductive disorder; an ovarian disorder; ovarian cancer;
 XX dysfunctional uterine bleeding; amenorrhoea; primary gynaecorrhoea;
 XX sexual dysfunction; infertility; pelvic inflammatory disease;
 XX endometriosis; placental aromatase deficiency; premature menopause;
 XX placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant
 XX androgen metabolism; aberrant onset of female puberty; aberrant showing
 XX of female primary sexual characteristics; aberrant showing of female
 XX secondary sexual characteristics; precocious puberty; precocious
 XX pseudopuberty; incomplete isosexual precocity; premature thelarche;
 XX premature adrenarche; premature pubarche; polycystic ovarian disease;
 XX aberrant ovarian cycle; menorrhagia; metrorrhagia; menometrorrhagia;
 XX dysmenorrhoea; hypomenorrhoea; polymenorrhoea; dysfunctional uterine
 XX bleeding; resistant-ovary syndrome; hermaphroditism; immune disorders;
 XX inflammatory disorders; arthritis; asthma; immunodeficiency diseases such
 XX as AIDS; leukaemia; rheumatoid arthritis; granulomatous disease;
 XX inflammatory bowel disease; sepsis; acne; neutropenia; neutrophilia;

CC psoriasis; hypersensitivities; such as T-cell mediated cytotoxicity;
 CC immune reactions to transplanted organs and tissues; such as host-versus-
 CC graft and graft-versus-host diseases; or autoimmune disorders;
 CC antihuman infertility; Addison's Disease; haemolytic anaemia;
 CC antiphospholipid syndrome; rheumatoid arthritis; dermatitis; allergic
 CC encephalomyelitis; glomerulonephritis; Goodpasture's Syndrome; Graves
 CC Disease; Multiple Sclerosis; Myasthenia gravis; Neuritis; Ophthalmia;
 CC Bullous Pemphigoid; Pemphigus; Polyendocrinopathies; Purpura; Reiter's
 CC Disease; Stiff-Man Syndrome; autoimmune thyroiditis; Systemic Lupus
 CC Erythematosus; Autoimmune Pulmonary Inflammation; Guillain-Barre Syndrome
 CC ; insulin dependent diabetes mellitus; autoimmune inflammatory eye
 CC disease; lens tissue injury; demyelination; systemic lupus erythematosus;
 CC drug induced haemolytic anaemia; rheumatoid arthritis; Sjogren's disease;
 CC and scleroderma. The present sequence is given in comparison with BGS-19
 CC in the present invention.

XX Sequence 697 AA;

XX Query Match 95.2%; Score 2576.5; DB 7; Length 697;

XX Best Local Similarity 73.0%; Pred. No. 7.4e-195;

XX Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

QY 1 MLLPLLSSLLGGSSQAMDGREWIRVQSSVMVPEGLCISVPCSPSYPRQDMTGSTPAYGW 60

DB 1 MLLPLLSSLLGGSSQAMDGREWIRVQSSVMVPEGLCISVPCSPSYPRQDMTGSTPAYGW 60

QY 61 FKAVTTTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGMCSLVIRDAQMDQESQYFVRV 120

DB 61 FKAVTTTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGMCSLVIRDAQMDQESQYFVRV 120

QY 121 ERGSYVRYNFMNDGFELKVTALTKQPDVYIPETLEPGQVTVICVFNWAECECPSPFSW 180

DB 121 ERGSYVRYNFMNDGFELKVTALTKQPDVYIPETLEPGQVTVICVFNWAECECPSPFSW 180

QY 181 TGAALSSQGTKPTTSHFSLVSFTPRPDQDHTDLCVDFSRKGVSAQRTVRLRVAYAPRD 240

DB 181 TGAALSSQGTKPTTSHFSLVSFTPRPDQDHTDLCVDFSRKGVSAQRTVRLRVAYAPRD 240

QY 241 LVISISRDNTPD----- 252

DB 241 LVISISRDNTPD----- 300

QY 253 -----PPENLRVMVSOANRTVLE 270

DB 301 WGPRLGLELPVYKAGSGRYTCAENRLGSGQALDLSVQYPENLRVMVSOANRTVLE 360

QY 271 NLNGTSLPVLEGSLCLVCTHSSPPARLSWTORGQVLSQSPQSDPGVLELPRVQVEHE 330

DB 361 NLNGTSLPVLEGSLCLVCTHSSPPARLSWTORGQVLSQSPQSDPGVLELPRVQVEHE 420

QY 331 GEFTCHARHPLGSGHVSLSLVHY----- 354

DB 421 GEFTCHARHPLGSGHVSLSLVHYFKLLGPPSCSWEAEGLHCSCSSQASAPSLRWLGE 480

QY 355 -----K 355

DB 481 ELLEGSSQDSFEVTPSSAGPWANSLSLRGLSSGLRLCEAMNVHGAQSGSLQLPDK 540

QY 356 KGLISTAFSNGAFGLIGITALLFLCLALIMKILPKRRTQTETPRFRSHSTILDYINV 415

DB 541 KGLISTAFSNGAFGLIGITALLFLCLALIMKILPKRRTQTETPRFRSHSTILDYINV 600

QY 416 VPTAGPLAQRNKAATNSPTPLPGAPSPESKKNQKQYQLPSPFPKSSTOAPESQ 475

DB 601 VPTAGPLAQRNKAATNSPTPLPGAPSPESKKNQKQYQLPSPFPKSSTOAPESQ 660

QY 476 SQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 512

DB 651 SQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 697

RESULT 5
AD137010

ID ADI37010 standard; protein; 697 AA.
XX
AC ADI37010;
XX
DT 22-APR-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO 71236.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2004004649-A2.
XX
PD 15-JAN-2004.
XX
PF 08-JUL-2003; 2003WO-US021083.
XX
PP 08-JUL-2002; 2002US-0394485P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld J, Wood W, Wu T;
XX
DR WPI; 2004-142912/14.
DR N-PSDB; ADI37009.
XX
PS Claim 10; SEQ ID NO 10; 118pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neurotrophic factors and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
XX
SQ Sequence 697 AA;
Query Match 95.2%; Score 2576.5; DB 8; Length 697;
Best Local Similarity 73.0%; Pred. No. 7.4e-195;
Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;
QY 1 MLLPLLLLSLLGGQMDGRFIRVOESVVMVEGLCISVPCSFSPQDWTGSTPAYGYW 60
DB 1 MLLPLLLLSLLGGQMDGRFIRVOESVVMVEGLCISVPCSFSPQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYVRYNFMNDGFFLKVTALTKQEDVYIPETLEPGQPVTVICVFNWAFESCPSPFSW 180
DB 121 ERGSYVRYNFMNDGFFLKVTALTKQEDVYIPETLEPGQPVTVICVFNWAFESCPSPFSW 180

QY 181 TGAALSSQGTPTTSFSLVSFTPRPDHDTLTCHVDFSRKGVSAQRTVLRVAYAPRD 240
DB 181 TGAALSSQGTPTTSFSLVSFTPRPDHDTLTCHVDFSRKGVSAQRTVLRVAYAPRD 240
QY 241 LVISIRSDNTPD----- 252
DB 241 LVISIRSDNTPALEPQPGNVVLEAQGOFLRLCAADSPATLSWVLRVLSLSSHP 300
QY 253 -----PPENLRVMVSOANRTVLE 270
DB 301 WGRPRGLGLPGVKAGDSGRVTCBAENRIGSQOQALDLSVQYPPENLRVMVSOANRTVLE 360
QY 271 NLNGTSLPVLGGOSLCLVCTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 330
DB 361 NLNGTSLPVLGGOSLCLVCTHSSPPARLSWTORGQVLSQSPSDPGVLELPRVQVEHE 420
QY 331 GEFTCHARHPLGSOHVSLSLVHY----- 354
DB 421 GEFTCHARHPLGSOHVSLSLVHYSPKLLGPSCSWEAEGLHCSCSSQASAPSLRWLGE 480
QY 355 -----X 355
DB 481 ELLEGSSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLRCEAMNVHGAQSGSILQLPDK 540
QY 356 KGLISTAFSNGAFUGIGITALLFLCLALIIIMKILPKERTOTETPRPFSRHSSTILDYINV 415
DB 541 KGLISTAFSNGAFUGIGITALLFLCLALIIIMKILPKERTOTETPRPFSRHSSTILDYINV 600
QY 416 VPTAGPLAQKENQKATPNSPRTPLPPGAPSPESKKNQKQYQVLPSPFPEPKSSTQAPESQE 475
DB 601 VPTAGPLAQKENQKATPNSPRTPLPPGAPSPESKKNQKQYQVLPSPFPEPKSSTQAPESQE 660
QY 476 SOEELHVTATLNPFPVRPPEARMKPGTQADYAEVKFQ 512
DB 661 SOEELHVTATLNPFPVRPPEARMKPGTQADYAEVKFQ 697
RESULT 6
ADL82805
ID ADL82805 standard; protein; 697 AA.
AC ADL82805;
DT 17-JUN-2004 (first entry)
DE Human PRO71236, SEQ ID 7.
KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
KW Gene Therapy; PRO; B cell related disorder; cancer;
KW immune-mediated inflammatory disease; human.
XX
OS Homo sapiens.
XX
PN WO2004024097-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029097.
XX
PR 16-SEP-2002; 2002US-0411392P.
XX
PA (GETH) GENENTECH INC.
XX
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
PI Wu TD;
XX
DR WPI; 2004-329389/30.
DR N-PSDB; ADL82804.
XX
PT New PRO polypeptide, useful for diagnosing and treating a B cell related
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.


```

61  FKAVTTTKGAPVATNHQSRREVMSRGRFQLTGDPKAGNCSLVIRDAQMDSQYFFRV 120
121 ERGSYVRYNFMNDGFLKVTALTQKEDVYIPETLEFGQPVTVICVFNWAFBESCPSPFSW 180
121 ERGSYVRYNFMNDGFLKVT-----140
181 TGAALSSQGTKPTTSHFSVLSFTPRQDHDITDCHVDSRKGVSQAQRTVRLVAVAPRD 240
141 -----VLSFTPRQDHDITDCHVDSRKGVSQAQRTVRLVAVAPRD 182
241 LVISISRDNTPD-----252
183 LVISISRDNTPALPEQPQGNVPLYEAQKQFLFLLCAADSPATLSWYLNQNRVLSSSH 242
253 -----PPENLRVWVQAQNTVLE 270
243 WGRPRPLGLELPGYKAGDSGRYTCEAENRLGSCQQRALDLSVOYPPENLRVWVQAQNTVLE 302
271 NLNGTSLPVLGQSILCLVCTHSSPPARLSWTQRCQVLSPSPQSPDPGVLELPRVQVEHE 330
303 NLNGTSLPVLGQSILCLVCTHSSPPARLSWTQRCQVLSPSPQSPDPGVLELPRVQVEHE 362
331 GFTCHARPLGSHVLSLSVHYKGLISTAFSGAFIGITALLFLCLALITMKILP 390
363 GFTCHARPLGSHVLSLSVHYKGLISTAFSGAFIGITALLFLCLALITMKILP 422
391 KRRTQETPRPRESRSTILDYINVVPTAGPLAQKRNQATPNSRPTPLPPGAPSPESKK 450
423 KRRTQETPRPRESRSTILDYINVVPTAGPLAQKRNQATPNSRPTPLPPGAPSPESKK 482
451 NQKKQYQLSPFPEPKSSTOAPESQESBETHVATLNFGRVPRPEARMKGTQADYAEVK 510
483 NQKKQYQLSPFPEPKSSTOAPESQESBETHVATLNFGRVPRPEARMKGTQADYAEVK 542
511 FQ 512
543 FQ 544

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RESULT 11

AAU29082
ID AAU29082 standard; protein; 544 AA.

AC AAU29082;

18-DEC-2001 (first entry)

Human PRO polypeptide sequence #59.

PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

Homo sapiens.

WO2001:68848-A2.

20-SEP-2001.

28-FEB-2001; 2001WO-US006520.

01-MAR-2000; 2000WO-US005601.

02-MAR-2000; 2000WO-US005841.

03-MAR-2000; 2000US-0187202P.

06-MAR-2000; 2000US-0186968P.

14-MAR-2000; 2000US-0189320P.

14-MAR-2000; 2000US-0189328P.

21-MAR-2000; 2000US-0066884.

21-MAR-2000; 2000US-0191007P.

21-MAR-2000; 2000US-0191048P.

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21-MAR-2000; 2000US-0191314P.
28-MAR-2000; 2000US-0192655P.
29-MAR-2000; 2000US-0193032P.
29-MAR-2000; 2000US-0193053P.
30-MAR-2000; 2000WO-US008439.
04-APR-2000; 2000US-0194449P.
04-APR-2000; 2000US-0194647P.
11-APR-2000; 2000US-0195975P.
11-APR-2000; 2000US-0196187P.
11-APR-2000; 2000US-0196690P.
11-APR-2000; 2000US-0196820P.
18-APR-2000; 2000US-0198121P.
18-APR-2000; 2000US-0198585P.
25-APR-2000; 2000US-0199397P.
25-APR-2000; 2000US-0199550P.
03-MAY-2000; 2000US-0199654P.
03-MAY-2000; 2000US-0201516P.
17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-JUN-2000; 2000WO-US015264.
05-JUN-2000; 2000US-0209832P.
28-JUL-2000; 2000WO-US020710.
22-AUG-2000; 2000US-00644848.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
01-DEC-2000; 2000WO-US032678.
20-DEC-2000; 2000WO-US034956.

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(GETH) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-602746/68.

N-PSDB; AAS45983.

Novel nucleic acids encoding PRO polypeptides, used to diagnose the
presence of tumors, such as prostate and breast tumors, in mammals and to
screen for modulators of the compounds.

Claim 11; Fig 118; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
The PRO polypeptides and their associated nucleic acids can be used to
detect the presence of a tumour in a mammal by comparing the level of
expression of a PRO polypeptide in a test sample of cells from the animal
and a control sample of normal cells, whereby a higher level of
expression in the test sample indicates the presence of a tumour in the
mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
and rabbits but are preferably human. The polypeptides can be used to
stimulate tumour necrosis factor (TNF) alpha release from human blood,
when contacted with it. A specific polypeptide can be used to stimulate
the proliferation or differentiation of chondrocyte cells. The PRO
proteins can be used to determine the presence of tumours and also
susceptibility to tumour development, particularly adrenal, lung, colon,
breast, prostate, cervical, or liver tumours, in mammalian
subjects. The oligonucleotide probes specific for the PRO nucleic acids
can be used for genetic analysis of individuals with genetic disorders

Sequence 544 AA;

Query Match 83.7%; Score 2265; DB 4; Length 544;

Best Local Similarity 74.8%; Pred. No. 2.4e-170;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy 1 MLLPLLSSLLGGSQAMDGFWIRVOESVWVPEGLCISVPCSFYPRQDWTSTPAYGW 60

Db 1 MLLPLLSSLLGGSQAMDGFWIRVOESVWVPEGLCISVPCSFYPRQDWTSTPAYGW 60

Qy 61 FKAVTTTKGAPVATNHQSRREVMSRGRFQLTGDPKAGNCSLVIRDAQMDSQYFFRV 120

Db 61 PKAVTETTKGAPVATNHOSREVMSTRGRFQITGDPKAGNCSLVIRDAQMDESOYFRV 120
QY 121 ERGSVVRNFNDGFFLKVTALTKQPDVYIETLEPGQPVTVICVFNWAFEECPFPFSW 180
Db 121 ERGSVTVTNFNDGFFLKVT ----- 140
QY 181 TGAALSSQTKFTTSHFSVLGFTPRPQDHTDLCHVDFSRKGSVAQRTVRLRVAYAPRD 240
Db 141 -----VLSTFRPQDHTDLCHVDFSRKGSVAQRTVRLRVAYAPRD 182
QY 241 LVISIRONTDP----- 252
Db 183 LVISIRONTALEPQPOQNVYLEAQKQFLRLICAADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVMYSQANRTVLE 270
Db 243 WQPRFLGLELPCVKAGDSGRVTCRAENRLGSOQRALDLSVQYPPENLRVMYSQANRTVLE 302
QY 271 NLNGTSLFVLEGQSLCLVCTHSHSPPARLSWTQRQVLSQPSQSDPGVLELPRVQVEHE 330
Db 303 NLNGTSLFVLEGQSLCLVCTHSHSPPARLSWTQRQVLSQPSQSDPGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSHVLSLSVHYKKGILSTAFSNGAFIGITALLFLCLALIMKILP 390
Db 363 GEFTCHARHPLGSHVLSLSVHYKKGILSTAFSNGAFIGITALLFLCLALIMKILP 422
QY 391 KRTQTETPRFRFSRHSHTILDYINVVPTAGPLAQRNOKATPNSRTPLPFGAPSPESKK 450
Db 423 KRTQTETPRFRFSRHSHTILDYINVVPTAGPLAQRNOKATPNSRTPLPFGAPSPESKK 482
QY 451 NOKKQVQLPSFPPEKPSSTQAPESQSBELHYATLNFPGVPRPRPEARMKGTQADYAEVK 510
Db 483 NOKKQVQLPSFPPEKPSSTQAPESQSBELHYATLNFPGVPRPRPEARMKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 12
ID ABUS8458 standard; protein; 544 AA.
XX AC ABUS8458;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #59.
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176492.
XX PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 18-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
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ABR66195

ID ABR66195 standard; protein; 544 AA.

XX

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XX 05-AUG-2003 (first entry)

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KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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PN 06-FEB-2003.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
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US-09-910-600-28

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QY 356 KGLISTAFNGAFGLGIGITALLELCIALIIMKILPKRTOTETPRFRSHSTILDYINV 415
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QY 416 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEPKSSTQAPESQ 475
DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEPKSSTQAPESQ 660
QY 476 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512
DB 661 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 2

US-09-984-130-149
Sequence 149, Application US/09984130
Publication No. US200305231A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PP489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 149
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-130-149

Query Match 95.2%; Score 2576.5; DB 10; Length 697;

Best Local Similarity 73.0%; Pred. No. 2e-177; 2; Indels 185; Gaps 2;
Matches 509; Conservative 1; Mismatches 2;

QY 1 MLLPLLSSLLGGSQAMDGRFWIRVQESVAVVPEGLCLISVPCSFSPRODMTGSTPAYGYW 60
DB 1 MLLPLLSSLLGGSQAMDGRFWIRVQESVAVVPEGLCLISVPCSFSPRODMTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGFTQLTGDPKAGNCSLVIRDAQMCDSQYFFRV 120
DB 61 FKAVTETTKGAPVATNHQSEVEMSTRGFTQLTGDPKAGNCSLVIRDAQMCDSQYFFRV 120
QY 121 ERGSYRYNFMNDGFLKVTALTCKPDVYIPETLEPGQVTVICVFNWAFEECPPEFSW 180
DB 121 ERGSYRYNFMNDGFLKVTALTCKPDVYIPETLEPGQVTVICVFNWAFEECPPEFSW 180
QY 181 TGAALSSQGTKPTTSHFSLVLSFTPRQDHTDITCHVDFSRKGVSAQRTVRLRVAYAPRD 240
DB 181 TGAALSSQGTKPTTSHFSLVLSFTPRQDHTDITCHVDFSRKGVSAQRTVRLRVAYAPRD 240
QY 241 LVTSISRDNTPD 252
DB 241 LVTSISRDNTPALEPQGNVPYLEAQKGQFLRLCAADSQPPATLSWVLQNRVLSSSH 300
QY 253 301 WGPRLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSOANRTVLE 360
QY 271 NLNGTSLPVLQGSCLVCTHSSPPARLSWTQGVLSPOSPDPGVLELPRVQVEHE 330
DB 361 NLNGTSLPVLQGSCLVCTHSSPPARLSWTQGVLSPOSPDPGVLELPRVQVEHE 420
QY 331 GEFTCHARHPLGSOHVSLSVHY 354
DB 421 GEFTCHARHPLGSOHVSLSVHYSKLLGPSCSWEAEGHLHCSSQASAPSLRWLGE 480
QY 355 481 ELLEGSSQDSFEVTPSSAGPWANSSLSLHGGSSGLRLRCEANVHGAQSGSILQLPDK 540
QY 356 KGLISTAFNGAFGLGIGITALLELCIALIIMKILPKRTOTETPRFRSHSTILDYINV 415
DB 541 KGLISTAFNGAFGLGIGITALLELCIALIIMKILPKRTOTETPRFRSHSTILDYINV 600
QY 416 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEPKSSTQAPESQ 475
DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEPKSSTQAPESQ 660
QY 476 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512
DB 661 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 3

US-10-403-938-7
Sequence 7, Application US/10403938
Publication No. US20040025195A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
TITLE OF INVENTION: BGS-19
FILE REFERENCE: D0227 NP
CURRENT APPLICATION NUMBER: US/10/403,938
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: U.S. 60/368,422
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 697
TYPE: PRT
ORGANISM: Homo sapiens
US-10-403-938-7

Query Match 95.2%; Score 2576.5; DB 15; Length 697;

Best Local Similarity 73.0%; Pred. No. 2e-177; 2; Indels 185; Gaps 2;
Matches 509; Conservative 1; Mismatches 2;

QY 1 MLLPLLSSLLGSGQAMGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
Db 1 MLLPLLSSLLGSGQAMGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
Db 61 FKAVTETTKGAPVATNHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYVRNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTIVCFNNAFEECPSPFSW 180
Db 121 ERGSYVRNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTIVCFNNAFEECPSPFSW 180
QY 181 TGAALSSQGTKTTHSFVLSFTPRQDHTDILCHVDPSRKGVSAQRTVRLRAYAPRD 240
Db 181 TGAALSSQGTKTTHSFVLSFTPRQDHTDILCHVDPSRKGVSAQRTVRLRAYAPRD 240
QY 241 LVISISRDNTPD----- 252
Db 241 LVISISRDNTPALEPQPOGNVPLEAQKQFLRLCAADSPATLSWVLRVLSSSH 300
QY 253 ----- 270
Db 301 WGRPLGLELPGVKAGDSGRYTCRAENRLGSGQORALDLSVQYPPENLRVMSQANRTVLE 360
QY 271 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSPQSDPGVLELPRVQVEHE 330
Db 361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSPQSDPGVLELPRVQVEHE 420
QY 331 GEFTCHARPLGSGHVLSLSVHY----- 354
Db 421 GEFTCHARPLGSGHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWLGE 480
QY 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEAMNVHGAQSGSILQLPDK 540
QY 356 KGLISTAFSNGAFIGITALLFLCLALIMKILPKRRTQETPRFRSHSTILDYINV 415
Db 541 KGLISTAFSNGAFIGITALLFLCLALIMKILPKRRTQETPRFRSHSTILDYINV 600
QY 416 VPTAGPLAQKRNQKATPNSPRTPLPGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQE 475
Db 601 VPTAGPLAQKRNQKATPNSPRTPLPGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQE 660
QY 476 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512
Db 661 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 4

US-10-614-853-10
; Sequence 10, Application US/10614853
; Publication No. US20040138114A1
; GENERAL INFORMATION:

; APPLICANT: HENRY CHIU
; APPLICANT: HILARY CLARK
; APPLICANT: KATHRYN DENNIS
; APPLICANT: SHERMAN FONG
; APPLICANT: JILL SCHOENFELD
; APPLICANT: WILLIAM WOOD
; APPLICANT: THOMAS WU

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
; TITLE OF INVENTION: RELATED DISEASES
; FILE REFERENCE: P1973R1-US
; CURRENT APPLICATION NUMBER: US/10/614,853
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/394,485
; PRIOR FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 28

; SEQ ID NO 10
; LENGTH: 697
; TYPE: PRT

; ORGANISM: Homo sapien
US-10-614-853-10

Query Match 95.2%; Score 2576.5; DB 16; Length 697;

Best Local Similarity 73.0%; Fred. No. 2e-177;

Matches 509; Conservative 1; Mismatches 2; Indels 185; Gaps 2;

QY 1 MLLPLLSSLLGSGQAMGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
Db 1 MLLPLLSSLLGSGQAMGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
Db 61 FKAVTETTKGAPVATNHQREVMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYVRNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTIVCFNNAFEECPSPFSW 180
Db 121 ERGSYVRNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTIVCFNNAFEECPSPFSW 180
QY 181 TGAALSSQGTKTTHSFVLSFTPRQDHTDILCHVDPSRKGVSAQRTVRLRAYAPRD 240
Db 181 TGAALSSQGTKTTHSFVLSFTPRQDHTDILCHVDPSRKGVSAQRTVRLRAYAPRD 240
QY 241 LVISISRDNTPD----- 252
Db 241 LVISISRDNTPALEPQPOGNVPLEAQKQFLRLCAADSPATLSWVLRVLSSSH 300
QY 253 ----- 270
Db 301 WGRPLGLELPGVKAGDSGRYTCRAENRLGSGQORALDLSVQYPPENLRVMSQANRTVLE 360
QY 271 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSPQSDPGVLELPRVQVEHE 330
Db 361 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTORGQVLSPQSDPGVLELPRVQVEHE 420
QY 331 GEFTCHARPLGSGHVLSLSVHY----- 354
Db 421 GEFTCHARPLGSGHVLSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWLGE 480
QY 355 -----K 355
Db 481 ELLEGNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEAMNVHGAQSGSILQLPDK 540
QY 356 KGLISTAFSNGAFIGITALLFLCLALIMKILPKRRTQETPRFRSHSTILDYINV 415
Db 541 KGLISTAFSNGAFIGITALLFLCLALIMKILPKRRTQETPRFRSHSTILDYINV 600
QY 416 VPTAGPLAQKRNQKATPNSPRTPLPGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQE 475
Db 601 VPTAGPLAQKRNQKATPNSPRTPLPGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQE 660
QY 476 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 512
Db 661 SQEELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 5

US-09-910-600-8
; Sequence 8, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:

; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8

LENGTH: 544

TYPE: PRT

ORGANISM: Homo sapiens

US-09-910-600-8

Query Match

84.2%; Score 2278; DB 10; Length 544;

Best Local Similarity 75.1%; Pred. No. 5.3e-156;

Matches 452; Conservative 1; Mismatches 1; Indels 148; Gaps 2;

1 MLLPLLLSLLGSGQAMGRFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTAYGVW 60

1 MLLPLLLSLLGSGQAMGRFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTAYGVW 60

61 FKAVTETTKAPVATNHQREVMSTGRFQLTGDPAKNCSLVIRDAQMDESQYFRV 120

61 FKAVTETTKAPVATNHQREVMSTGRFQLTGDPAKNCSLVIRDAQMDESQYFRV 120

121 ERGSYVRYNFMNDGFFLKVTALTKQPDVYIPETLEPGQPVTVICVFNWAFESCPSFSW 180

121 ERGSYVRYNFMNDGFFLKVT----- 140

181 TGAALSSQGTPTTSHFSVLSTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240

141 -----VLSTFTPRQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

241 LVLSISRDNTPD----- 252

183 LVLSISRDNTPALPEPOQGNVPYLEAQKQFLLLCAADSPPATLSWYLNKRVLSSHP 242

253 -----PPENLRVWVSOANRTVLE 270

243 WGRPRGLGLPVGKAGDSGRYTCRAENRLGSCQALDLSVQYFPPENLRVWVSOANRTVLE 302

271 NLNGTSLPVEGQSCLVCVTHSSPRLSWTORQVLSQPSQSDPGVLELPRVQVHE 330

303 NLNGTSLPVEGQSCLVCVTHSSPRLSWTORQVLSQPSQSDPGVLELPRVQVHE 362

331 GEFTCHARPLGSGVLSLVHYKGLISTAFSGAFIGITALLFLCLALIMKILP 390

363 GEFTCHARPLGSGVLSLVHYKGLISTAFSGAFIGITALLFLCLALIMKILP 422

391 KRRTQETPRPFSRHSITLDYINVVPTAGPLAQKRNQKATNSPRTPLPGAPSPESKK 450

423 KRRTQETPRPFSRHSITLDYINVVPTAGPLAQKRNQKATNSPRTPLPGAPSPESKK 482

451 NKKQYOLSPFPPKSGSTQAPESQESLHVATLNFGRVPRPERBMPKGTQADYAEVK 510

483 NKKQYOLSPFPPKSGSTQAPESQESLHVATLNFGRVPRPERBMPKGTQADYAEVK 542

511 FQ 512

543 FQ 544

RESULT 6

US-09-978-295A-259

Sequence 259, Application US/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194

QY 391 KRRTQTETPRFHSRHSHTILDYINVVPTAGPLAQKQKATNSPRTPLPPGAPSPESKK 450
DB 423 KRRTQTETPRFHSRHSHTILDYINVVPTAGPLAQKQKATNSPRTPLPPGAPSPESKK 482
QY 451 NKKQYQLSPFPBKSTQAPSQESQEBLHVATLNFPGVRPRPMPKGTQADYAEVK 510
DB 483 NKKQYQLSPFPBKSTQAPSQESQEBLHVATLNFPGVRPRPMPKGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544

RESULT 7

US-09-978-697-259
Sequence 259, Application US/09978697

Patent No. US20020163284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Agids Encoding the Same
FILE REFERENCE: P2630PIC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700

/ PRIOR FILING DATE: 1998-04-22
 / PRIOR APPLICATION NUMBER: 60/082797
 / PRIOR FILING DATE: 1998-04-22
 / PRIOR APPLICATION NUMBER: 60/082796
 / PRIOR FILING DATE: 1998-04-23
 / PRIOR APPLICATION NUMBER: 60/083336
 / PRIOR FILING DATE: 1998-04-27
 / PRIOR APPLICATION NUMBER: 60/083322
 / PRIOR FILING DATE: 1998-04-28
 / PRIOR APPLICATION NUMBER: 60/083392
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083495
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083496
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083499
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083545
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083554
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083558
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083559
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083500
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083742
 / PRIOR FILING DATE: 1998-04-30
 / PRIOR APPLICATION NUMBER: 60/084366
 / PRIOR FILING DATE: 1998-05-05
 / PRIOR APPLICATION NUMBER: 60/084414
 / PRIOR FILING DATE: 1998-05-06
 / PRIOR APPLICATION NUMBER: 60/084441
 / PRIOR FILING DATE: 1998-05-06
 / PRIOR APPLICATION NUMBER: 60/084637
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084639
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084640
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084598
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084600
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 / PRIOR FILING DATE: 1998-05-07
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 / PRIOR FILING DATE: 1998-05-13
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085700
 / PRIOR FILING DATE: 1998-05-15
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 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085579
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085580
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085704
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 9; Length 544;
 Best Local Similarity 74.8%; Pred. No. 4.6e-155;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;
 QY 1 MLLPLLSSLLGGSQAMDGFRFWIRVOESVMVPEGLCISVPCSFSPYPRQDWTGTPAYGW 60
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 Db |||||
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 QY 121 ERGSYRYNFMNDGFFLKVTALTQKPDVYIPETLEFGQPVTVCVFNWAFEECPSPFSW 180
 Db |||||
 Db 121 ERGSYRYNFMNDGFFLKVT----- 140
 QY 181 TGAALSSQGTKPTTSHFSLVSTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
 Db |||||
 Db 141 -----VLSTPRPDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
 QY 241 LVISISRDNTPD----- 252
 Db 183 LVISISRDNTPALEPOQGNVYLEAQKQFLLCALDLSVOYPPENLRVMVSOANRTVLE 242
 QY 253 -----PPENLRVMVSOANRTVLE 270
 Db 243 WGPRLGLELPGVKAGDSGRYTCAENRLGSOQOALDLSVOYPPENLRVMVSOANRTVLE 302
 QY 271 NLNGTSLPVLEQCSLVCVTHSSPPARLSWTORGVLSPSPQSPDFGVLELPRVQVEHE 330
 Db 303 NLNGTSLPVLEQCSLVCVTHSSPPARLSWTORGVLSPSPQSPDFGVLELPRVQVEHE 362
 QY 331 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIWKILP 390
 Db 363 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFIGITALLFLCLALIWKILP 422
 QY 391 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKQKATNSPRTPLPPGAPSPESKK 450
 Db 423 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKQKATNSPRTPLPPGAPSPESKK 482
 QY 451 NQKKQYQLPSFPFKSSTQAPESQESQELHYATLNFPGVRPPEARMKGTQADYAEVK 510
 Db 483 NQKKQYQLPSFPFKSSTQAPESQESQELHYATLNFPGVRPPEARMKGTQADYAEVK 542
 QY 511 FQ 512
 Db 543 FQ 544
 RESULT 8
 US-09-978-192A-259
 / Sequence 259, Application US/09978192A
 / Patent No. US20020177553A1
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleon
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Hillan, Kenneth J.
 / APPLICANT: Kljavin, Ivar J.
 / APPLICANT: Kuo, Sophia S.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James;
 / APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William L.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 9; Length 544;

Best Local Similarity 74.8%; Pred. No. 4, 6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLGSGQAMGRFIRVQESVMVPEGLICISVPCSFSPRODWTGSPAYGYW 60
DB 1 MLPLLLSLGSGQAMGRFIRVQESVMVPEGLICISVPCSFSPRODWTGSPAYGYW 60
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DB 61 FXAVTETTKGAVATNHQSRVEMSTRGFTQTPAKGNCSLVIRDAQMDQESYFFRV 120
QY 121 ERGSYRVNFMNDGFLLKYVLTALQKPDVYIPETLEPGQPVTVICVFNWAFECPPSPSW 180
DB 121 ERGSYRVNFMNDGFLLKYVLTALQKPDVYIPETLEPGQPVTVICVFNWAFECPPSPSW 180
QY 181 TGAALSSQGTKEKTTSHFSVLSFTPRPDHDTDLTCHVDPSRKVSAQRTVRLVAYAPRD 240
DB 141 -----VLSFTPRPDHDTDLTCHVDPSRKVSAQRTVRLVAYAPRD 182
QY 241 LVISIRDNTPD----- 252
DB 183 LVISIRDNTPALEPQPGNVPLYEAQKQFLRLICAADSQPPATLSVLQNRVLSSSH 242
QY 253 -----PPENLRVMVSOANRTVLE 270
DB 243 WGRPLGLPLGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVSOANRTVLE 302
QY 271 NLNGTSLVPLVGGSLCLVCTVTHSSPPARLSTQGVLSQSDPGVLELPRVQVEHE 330
DB 303 NLNGTSLVPLVGGSLCLVCTVTHSSPPARLSTQGVLSQSDPGVLELPRVQVEHE 362
QY 331 GEFTCHARPLGSHVLSLSVHYKGLISTAFSNGAFGLIGITALLFLCLALIMKILP 390
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DB 423 KRTOTETPRPFRSHSTILDVNVVPTAGPLAQKRNOKATNSPRTPLPCGAPSPESKK 482
QY 451 NOKKQYQLPSFPKSKSTQAPESQESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVK 510

DB 483 NOKKQYQLPSFPKSKSTQAPESQESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVK 542
QY 511 FQ 512
DB 543 FQ 544
RESULT 9
US-09-999-832A-259
; Sequence 259, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1063
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 9; Length 544;

Best Local Similarity 74.8%; Pred. No. 4,6e-155; Mismatches 3; Indels 148; Gaps 2;
Matches 450; Conservative 1;

Qy 1 MLPLLLSLGGQAMDFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTPAYGW 60
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Db 1 MLPLLLSLGGQAMDFWIRVOESVWVPEGLCISVPCSFSPRODWTGSTPAYGW 60
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Qy 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKGNCSLVIRDAQXQDESQYFFRV 120

Db 61 FNAVETTKGAPVATHQSRVEMSTRGRFQITGPAKNGSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYRVNFMNDGFFLKVTALTQKPDVYIPETLEFGQPVTVICVENWAFEECPPPFSW 180
Db 121 ERGSYRVNFMNDGFFLKVT----- 140
QY 181 TGAALSSQGTKTTHSHFSLFTPPQDHTDLTCHVDPSRKGVSQAQTVLRLVAYAPRD 240
Db 141 ----- 182
QY 241 LVISIRSDNTP----- 252
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Db 363 GBFTCHARPLGSHVLSLSVHYKKGLISTAFSGAFGLGITALLFLCLALIMKILP 422
QY 391 KRTOTETPRPFRSHSTILDVINVPTAGPLAQKRNOKATNSPRTPLPGCAPSPESKK 450
Db 423 KRTOTETPRPFRSHSTILDVINVPTAGPLAQKRNOKATNSPRTPLPGCAPSPESKK 482
QY 451 NQKQVQLPSPFPEKPSQESQBELHYATLNFQGVPRPRPARKGTQADYAEVK 510
Db 483 NQKQVQLPSPFPEKPSQESQBELHYATLNFQGVPRPRPARKGTQADYAEVK 542
QY 511 FQ 512
Db 543 FQ 544

RESULT 10

US-09-978-189-259
; Sequence 259, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;
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Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

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DB 1 MLLPLLSSLLGSSQAMDGFWIRVOESVMVPSGLCISVPCSFYPRQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNEQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDSSQYFFRV 120
DB 61 FKAVTETTKGAPVATNEQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDSSQYFFRV 120
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DB 121 ERGSYVYVNFMDGFFLKVTALTQKPDVYIPELEPQOPVTVICVFNWAFEECPFSPSW 180
QY 181 TGAALSSQGTKPTTSHPSVLSFTPRQDHDITDCHVDFSRKGVSAQRTVRLVAVAPRD 240
DB 141 -----VLSFTPRQDHDITDCHVDFSRKGVSAQRTVRLVAVAPRD 182
QY 241 LVISIRSDNTPD----- 252
DB 183 LVISIRSDNTPALEPQPGNVPLYEAKGQFLRLCAADSQPPATLSWVLQNRVLSSSH 242
QY 253 -----PPENLRVMVSQANRTVLE 270
DB 243 WGRPPLGLELPVGVKAGDSGRYTCRAENRLGSSQQRALDLSVQYPPENLRVMVSQANRTVLE 302
QY 271 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSPPSPQSPGVLELPRVQVEHE 330
DB 303 NLNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSPPSPQSPGVLELPRVQVEHE 362
QY 331 GEFTCHARHPLGSHVSLSVHYKGLISTAFNSGAFIGITALLFLCLALIMKILP 390
DB 363 GEFTCHARHPLGSHVSLSVHYKGLISTAFNSGAFIGITALLFLCLALIMKILP 422
QY 391 KRTQTETPRFRSRHSTILDYINVVPTAGLQAKNQKATNSPRTPLPPGAPSPESKK 450
DB 423 KRTQTETPRFRSRHSTILDYINVVPTAGLQAKNQKATNSPRTPLPPGAPSPESKK 482
QY 451 NQKKYQLPSFPFPKSTQAPESQESQELHYATLNFPGVYRPRPEARMKGTQADYAEVK 510
DB 483 NQKKYQLPSFPFPKSTQAPESQESQELHYATLNFPGVYRPRPEARMKGTQADYAEVK 542
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RESULT 11
US-09-978-608A-259
; Sequence 259, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-259
Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLLGSGQAMDFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLLGSGQAMDFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60

QY 61 FRAVETTTKGPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FRAVETTTKGPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120

QY 121 ERGSYRYNFMNDGPFLLKVTALTKQPDVYIPTELPFGQPVTVICVFNWAFEECPPPSPSW 180
DB 121 ERGSYRYNFMNDGPFLLKVT-----VLSTFPREPQDNTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 182

QY 181 TGAALSSQGTKPTTSHFSVLSTPRPDHDTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 240
DB 141 -----VLSTFPREPQDNTDLTCHVDFSRKGVSAQRTVRLVAVAPRD 182

QY 241 LVISISRDNTPD----- 252
DB 183 LVISISRDNTPALEPQPGNVPLYEAQKGFLLCAADSQPPATLSWLVQNRVLSSHP 242

QY 253 -----PPENLRVMVSCANRTVLE 270
DB 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSCANRTVLE 302

RESULT 12
US-09-978-585A-259
; Sequence 259, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-259
Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY 1 MLPLLLSLLGSGQAMDFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLLGSGQAMDFWIRVQESVMVPEGLCISVPCSFSPRQDWTGSTPAYGYW 60
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61 FXAVTETTKGAPVATNNHQSREVMSTGRGRPOLTGDPKAGNCSLVIRDAQWQDESQYFFRV 120
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121 ERGSYVYNNFMNDGFLKVTALTKQKDVVYIPETLPGQPVTVICVFNWAFESCEPPSPSM 180
121 ERGSYVYNNFMNDGFLKVT----- 140
181 TGAALSSQGTKPTTSHFSVLSTPRQDHDYDLCVDFSRKGVSAQRTVRLVAVAPRD 240
141 -----VLSFTPRQDHDYDLCVDFSRKGVSAQRTVRLVAVAPRD 182
241 LVISISRDNTPD----- 252
183 LVISISRDNTPALEPOQGNVPLYEAQKQGLFLLCAASQBPATLSWVLQNRVLSSSH 242
253 -----PPENLRVWVSQANRTVLE 270
243 WGRPLGLEPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVWVSQANRTVLE 302
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RESULT 13
US-09-937-191A-259
Sequence 259, Application US/09978191A
Publication No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/084598
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; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07

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; PRIOR APPLICATION NUMBER: 60/084627
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; PRIOR APPLICATION NUMBER: 60/085339
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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 83.7%; Score 2265; DB 10; Length 544;

Best Local Similarity 74.8%; Pred.No. 4.6e-155;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

Qy 1 MLLPLLSSLLGGQAMDFWIRVQESVMVPEGLCLISVPCSFSPYQDWTGSTPAYGYW 60
Db 1 MLLPLLSSLLGGQAMDFWIRVQESVMVPEGLCLISVPCSFSPYQDWTGSTPAYGYW 60
Qy 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVR 120
Db 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFVR 120
Qy 121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETILEPGQPVTVCVFNWAFEECPPPFSW 180
Db 121 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETILEPGQPVTVCVFNWAFEECPPPFSW 180
Qy 181 TGAALSQGTKPTTSHPSVLSFTPRPDQDHTDLTCHVDFSRKGVSQRTVRLRVAYAPRD 240
Db 141 -----VLSFTPRPDQDHTDLTCHVDFSRKGVSQRTVRLRVAYAPRD 182
Qy 241 LVISISRDNTPD----- 252
Db 183 LVISISRDNTPALEFPQGNVPYLEAQGFRLLLCAADSQPFATLSWVLQNRVLSSSH 242
Qy 253 -----PPENLRVMVSOANRTVLE 270
Db 243 WGRPLGLELPGVKAGDSGRYTCAENRLGSOQBALDLSVQYPPENLRVMVSOANRTVLE 302
Qy 271 NLNGTSLPVLEGGQSLCLVCVTHSSPPARLSWTQRGVLSQPSQSPDGVLELPRVQVEHE 330
Db 303 NLNGTSLPVLEGGQSLCLVCVTHSSPPARLSWTQRGVLSQPSQSPDGVLELPRVQVEHE 362
Qy 331 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFLGIGITALLFLCLALLIMKILP 390
Db 363 GEFTCHARHPLGSHVLSLSVHYKGLISTAFSNGAFLGIGITALLFLCLALLIMKILP 422
Qy 391 KRRQTETTPRFRSHSTILDYINVVFTAGFLAQRNOKATPNSRPTLPFGAPSPESKK 450
Db 423 KRRQTETTPRFRSHSTILDYINVVFTAGFLAQRNOKATPNSRPTLPFGAPSPESKK 482
Qy 451 NQKQYQLPSPPPKSSTQAPESQSEELHYATLNFPGVRPEARMKPGTQADYAEVK 510
Db 483 NQKQYQLPSPPPKSSTQAPESQSEELHYATLNFPGVRPEARMKPGTQADYAEVK 542
Qy 511 FQ 512
Db 543 FQ 544

RESULT 14

US-09-978-403A-259

Sequence 259, Application US/09978403A

Publication No. US20030050240A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
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PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26

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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495

Query Match 83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred.No. 4.6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 149; Gaps 2;

Qy 1 MLPLLLSLGSGQAMDCRFWRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTAYGYW 60
Db 1 MLPLLLSLGSGQAMDCRFWRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTAYGYW 60

Qy 61 FKAIVTTTGGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRV 120
Db 61 FKAIVTTTGGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRV 120

Qy 121 ERGSVYVTFMNDGFFLKVT----- 140

Db 121 ERGSVYVTFMNDGFFLKVT----- 140

Qy 181 TGAALSSQGIKPTTSHFSVLSFTPRPODHTDLTCHVDPSRKGVSQRTVLRVAYAPRD 240

Db 141 -----VLSFTPRPODHTDLTCHVDPSRKGVSQRTVLRVAYAPRD 182

Qy 241 LVISISRDNTPD----- 252

Db 183 LVISISRDNTPALEPQPGNVVYLEAQKGQFLRLCAADSQPPATLSWVLRVLSSSH 242

Qy 253 -----PENLRVMVQANRTVLE 270

Db 243 WGRPLGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVOYPPENLRVMVQANRTVLE 302

Qy 271 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQRGOVLSPSQSPSDPGVLELRVQVEHE 330

Db 303 NLNGTSLPVLGOSLCLVCVTHSSPPARLSWTQRGOVLSPSQSPSDPGVLELRVQVEHE 362

Qy 331 GEFTCHARHPLGSHVSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIMKILP 390

Db 363 GEFTCHARHPLGSHVSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIMKILP 422

Qy 391 KRRQTETPRFRSRHSTILDYINVVPTAGTACKRQKATPNSPRTPLEPPGAPSPSKK 450

Db 423 KRRQTETPRFRSRHSTILDYINVVPTAGTACKRQKATPNSPRTPLEPPGAPSPSKK 482

Qy 451 NQKQYQLPSPPEPKSTQAPESQSEELHYATLNPFGVRPPEARMPKGTQADYAEVK 510

Db 483 NQKQYQLPSPPEPKSTQAPESQSEELHYATLNPFGVRPPEARMPKGTQADYAEVK 542

Qy 511 FQ 512

Db 543 FQ 544

RESULT 15

US-09-978-564A-259
; Sequence 259, Application US/09978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

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; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C25

; CURRENT APPLICATION NUMBER: US/09/978,564A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30	PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-04-08	PRIOR APPLICATION NUMBER: 60/081071
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      83.7%; Score 2265; DB 10; Length 544;
Best Local Similarity 74.8%; Pred. No. 4,6e-155;
Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps 2;

QY      1 MLLPILLSLLGSGQAMGDFWIRVQESVMVEGLCISVPCSFSPRODWTGSTPAYGYW 60
DB      1 MLLPILLSLLGSGQAMGDFWIRVQESVMVEGLCISVPCSFSPRODWTGSTPAYGYW 60

QY      61 FXAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKGNCSLVIRDAQMDQESQYFFRV 120
DB      61 FXAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKGNCSLVIRDAQMDQESQYFFRV 120

QY      121 ERGSVYVYVNFMDGFLKVTALTQKPDVYIPETLBPQPVTVICVFNWAFBECPPSPSW 180
DB      121 ERGSVYVYVNFMDGFLKVT----- 140

QY      181 TGAALSSQGTKEPSSHFSVLSFTPRPQDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
DB      141 -----VLSTPRPQDHDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182

QY      241 LVISISRDNTPD----- 252
DB      183 LVISISRDNTPALEPOQGNVFLYEAQKQFLRLICAADSPATLSWYLQNRVLSSSH 242

QY      253 -----PPENLRVMVSOANRTVLE 270
DB      243 WGRPLGLLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSOANRTVLE 302

QY      271 NLGNGTSLPVLGQSCLVCVTHSSPPARLSWTQRQVLSQSPQSDPGVLELPRVQVEHE 330
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QY      331 GEFTCHARPLGSOHVLSLSVHYKKGLISTAFSGARLIGITALLFLCLALIIMKILP 390
DB      363 GEFTCHARPLGSOHVLSLSVHYKKGLISTAFSGARLIGITALLFLCLALIIMKILP 422

QY      391 KRRTQTETPRFRFSRHSHTILDYINVVPTAGPLAQKRNQKATNSPRTPLPPGAPSPESKK 450
DB      423 KRRTQTETPRFRFSRHSHTILDYINVVPTAGPLAQKRNQKATNSPRTPLPPGAPSPESKK 482

QY      451 NQKKQVQLSPFPKPSSTOAPESQESQELHYATLNFPGVRRPRPEARMKGTQADYAEVK 510
DB      483 NQKKQVQLSPFPKPSSTOAPESQESQELHYATLNFPGVRRPRPEARMKGTQADYAEVK 542

QY      511 FQ 512
DB      543 FQ 544
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Search completed: November 5, 2004, 14:13:46
Job time : 92.0765 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 17.7654 Seconds
(without alignments)
3460.797 Million cell updates/sec

Title: US-09-937-636-4
Perfect score: 3377
Sequence: 1 MLLPLLSSLLGSSQAMDGR.....RPEARMKGTQADYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	14.4	626	A61084	myelin-associated
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3	469.5	13.9	582	BNRT3S	myelin-associated
4	466.5	13.8	637	B33785	myelin-associated
5	451.5	13.4	364	A30521	myeloid cell surfa
6	392	11.6	620	JH0593	Schwann cell myeli
7	368	10.9	403	I52590	m33-B isoform - mo
8	311	9.2	862	I43583	differentiation an
9	305.5	9.0	868	A45112	CD22 homolog/8 lym
10	289.5	8.6	847	JH0371	B-cell adhesion pr
11	282.5	8.4	1694	S50065	sialoadhesin - mou
12	255	7.6	4391	A38096	perlecan precursor
13	251.5	7.4	628	I38000	Lutheran blood gro
14	245	7.3	648	A35648	B-cell adhesion pr
15	239.5	7.1	588	I37202	B-CAM protein - hu
16	236.5	7.0	761	IJHUNG	neural cell adhesi
17	235	7.0	725	IJHUNG	neural cell adhesi
18	235	7.0	858	IJHUNG	neural cell adhesi
19	235	7.0	1115	IJHUNG	biliary glycoprote
20	231.5	6.9	526	A32164	hypothetical prote
21	226.5	6.7	575	T26992	hemictin precurs
22	226.5	6.7	5198	T43290	telencephalin prec
23	226	6.7	917	I48950	heparan sulfate pr
24	226	6.7	3707	S18252	nephlin - human
25	225	6.7	1241	T37190	nephlin - human
26	224	6.6	853	IJBONC	neural cell adhesi
27	223.5	6.6	811	A41054	fasciclin II, tran
28	223.5	6.6	873	B41054	fasciclin II PI-li
29	218.5	6.5	1091	IJCHNL	neural cell adhesi

transient axonal g
axonal glycoprotei
protein-tyrosine k
transmembrane carc
vascular cell adhe
connectin/titin -
biliary glycoprote
connectin 3B - chi
biliary glycoprote
carcinoembryonic a
elastic titin - hu
protein-tyrosine-p
pregnancy-specific
fasciclin II precu
neural cell adhesi
probable neural ce

30 214 6.3 1040 2 A49356
31 211 6.2 1040 2 A34695
32 210 6.2 1070 2 JC4593
33 206 6.1 464 2 C30127
34 204.5 6.1 538 2 JC3457
35 203 6.0 462 2 T45633
36 201.5 6.0 458 2 JC1509
37 201 6.0 1323 2 PNO568
38 200.5 5.9 521 2 S34338
39 200.5 5.9 702 2 A36319
40 199.5 5.9 7962 2 I38346
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42 197 5.8 435 2 D33258
43 197 5.8 898 2 A40114
44 196 5.8 1092 1 JN0635
45 195.5 5.8 1209 2 T42718

ALIGNMENTS

RESULT 1
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myelin-associated glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: A61084; A33263; PC2011
R:Spagnol, G.; Williams, M.; Srinivasan, J.; Golier, J.; Bauer, D.; Lebo, R.V.; Latov, N.
J. Neurosci. Res. 24, 137-142, 1989
A:Title: Molecular cloning of human myelin-associated glycoprotein.
A:Reference number: A61084; MUID:90064604; PMID:2479762
A:Accession: A61084
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-626 <SPA>
A:Cross-references: UNIPROT:P20916
R:Sato, S.; Fujita, N.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Takahashi, Y.; Miyatake, Biochem. Biophys. Res. Commun. 163, 1473-1480, 1989
A:Title: cDNA cloning and amino acid sequence for human myelin-associated glycoprotein.
A:Reference number: A33263; MUID:89392083; PMID:2476987
A:Accession: A33263
A:Molecule type: mRNA
A:Residues: 1-613, 'T', 615-626 <SAT>
A:Cross-references: GB:M2973; NID:G187292; PIDN:AAA59545.1; PID:G307156
R:Burger, D.; Pidoux, I.; Steck, A.J.
Biochem. Biophys. Res. Commun. 197, 457-464, 1993
A:Title: Identification of the glycosylated sequons of human myelin-associated glycoprotein
A:Reference number: PC2011; MUID:94092116; PMID:7505568
A:Accession: PC2011
A:Molecule type: protein
A:Residues: 84-98, 'X', 100-110; 210-222, 'X', 224; 245, 'X', 247-253; 309-318, 'XXX'; 396-405, 'X', 4
C:Comment: This protein is a neural cell adhesion molecule.
C:Genetics:
A:Gene: GDB:MAG; GMA
A:Cross-references: GDB:I20702; OMIM:159460
A:Map position: 19q13.1-19q13.1
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: brain; cell adhesion; glycoprotein; phosphoprotein; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-626/Product: myelin-associated glycoprotein #status predicted <MAT>
F:35-102/Domain: immunoglobulin homology <IMM>
F:118-120/Region: cell attachment (R-G-D) motif
F:514-536/Domain: transmembrane #status predicted <TM>
F:99, 223, 246, 315, 406, 450, 454/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:106/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:332/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:543, 607/Binding site: phosphate (Thr) (covalent) #status predicted
F:573/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 14.4%; Score 487; DB 1; Length 626;
Best Local Similarity 23.9%; Pred. No. 2.4e-24;
Matches 169; Conservative 100; Mismatches 256; Indels 182; Gaps 19;

Db 188 RLREDEGTWQVSLHLLHVPFTRANGHRLGCOAAPNTTLQEGYASLDVKYPP--VIVEM 245
QY 188 SRDNTPALEPQGNVPLEAKQGFLLCAADSQPATLSVLQNRVLSHHPWGRPP 247
Db 246 NSS-----VEAIEGSHVSLLCGADSNPPPLLTWMDGMYLREA---VAES 287
QY 248 LGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVNVMSQANRTVLENLGN 307
Db 288 LYLDEEVTPAEDGIYACLAENAYQDNRTVELSVMYAPWKPVT-----NG 333
QY 308 TSLPVLGQSLCLVCTVTHSSPPARLSWTQGVLSFSPQSDPGVLELPRVQVEHEGFTC 367
Db 334 TVAV-EGEVTSLGTSQSNPDPIITFKKQILATVYESQLQLELPAVTPDDGGEYWC 392
QY 368 HARHPLGSHVLSLSVHYSPKLLGPS-CSWEAEGHLCSCSQASPAPSLRWMLGEELE 426
Db 393 VAENQYQGRATAFNLSVFPAPILLESCHCAARDVQCLCVKSNPESVAFELPSRNV 452
QY 427 GNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEAWNVHGAQSGSIQLPKKGLI 486
Db 453 VNETEREF-VYSESGLLTSLTRGQAQAPPRVICTSRNLYGTQS---LPLP----- 502
QY 487 STAFSNG-----AFIGIGITALLFLCLALIMKILPKERTQTETPRPFSHSITLDVIN 541
Db 503 ---FOGAHRLMWAIGPVGAVFAILIAIVCYITQTRKKNVTSPSFS----- 549
QY 542 VVPTAGPLAKENKATNPSRTPPLP-----GAPSP-ESKKNQKQYQLPSFPBPKSST 595
Db 550 ----AG-----DNPHVLSPEPRISGAPDKYSEKRLGSRRLGL----- 586
QY 596 QAPESQSEEBHYATNLNPGVVRPPEARMKGTQADVAEVK 637
Db 587 ---RGEPPDLDSYSHSDL-GKRPTKDSYTLTEELAEVAEIR 624

RESULT 3

BNRT3S
myelin-associated glycoprotein precursor, short splice form - rat
N:Alternate names: 1B236; brain neuron cytoplasmic protein 3; MAG
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1990 #sequence revision 30-Jun-1990 #text_change 16-Jun-2000
C:Accession: B29028; B27185; A60055
R:Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 4337-4341, 1987
A:Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule for
A:Reference number: A29028; MUID:87232001; PMID:2438699
A:Accession: B29028
A:Molecule type: mRNA
A:Residues: 1-582 <LAI>
A:Cross-references: GB:M22357; NID:g205271; PIDN:AAA41558.1; PID:g205272
R:Salter, J.L.; Holmes, W.P.; Colman, D.R.
J. Cell Biol. 104, 957-965, 1987
A:Title: The amino acid sequences of the myelin-associated glycoproteins: homology to th
A:Reference number: A27185; MUID:87166195; PMID:2435742
A:Accession: B27185
A:Molecule type: mRNA
A:Residues: 419-582 <SAL>
A:Cross-references: GB:X06554; NID:956614; PIDN:CAA29797.1; PID:g1334302
R:Tropak, M.B.; Johnson, P.W.; Dunn, R.J.; Roder, J.C.
Brain Res. Mol. Brain Res. 4, 143-155, 1988
A:Title: Differential splicing of MAG transcripts during CNS and PNS development.
A:Reference number: A60055
A:Accession: A60055
A:Molecule type: mRNA
A:Residues: 565-582 <TRO>
C:Comment: The sequence contains five presumably extracellular domains that are distantl
C:Comment: The short form is found in the adult; the long form predominates in early pos
C:Genetics:
A:Gene: MAG
A:Map position: 7
C:Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; trans
F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-582/Product: myelin-associated glycoprotein, short splice form #status predicted <M
F:35-102/Domain: immunoglobulin homology <IMM1>
F:118-120/Region: cell attachment (R-G-D) motif
F:219-219/Domain: immunoglobulin homology <IMM2>
F:254-307/Domain: immunoglobulin homology <IMM3>
F:340-394/Domain: immunoglobulin homology <IMM4>
F:425-490/Domain: immunoglobulin homology <IMM5>
F:514-536/Domain: transmembrane #status predicted <TM>
F:537-582/Domain: intracellular #status predicted <INT>
F:99,223,246,315,332,406,450,454/Binding site: carbohydrate (Asn) #status prec

Query Match 13.3%; Score 469.5; DB 1; Length 582;
Best Local Similarity 24.7%; Pred. No. 38-23;
Matches 146; Conservative 89; Mismatches 226; Indels 129; Gaps 13;

QY 21 FWIRVQ-----ESWVPEGLICISVPCSFSPRODWTGSTPAYGVFKAVTETT 68
Db 10 FWMISASRGHWGAWMPSSISAFEGTCVSIKCFDPP--DELPAVHVGVVFNPSYPK 67
QY 69 KGAPVATNHQSREVEMSTRGRFOLTGDPKAGKNSLVIRDAQMDQESQYFFRVERGSVRY 128
Db 68 NYPVVPFKSRTOVVHESFQGRSRLLDGLGRNCTLLSTLSPELGKGYPRGLGGYNOY 127
QY 129 NFM----- 131
Db 128 TFSEHSLDIINTPNIVVPPEVAGVEVSCVMPDNCPELRPELSWLGHEGEPVLG 187
QY 132 ---NDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPDLVISI 187
Db 188 RLREDEGTWQVSLHLLHVPFTRANGHRLGCOAAPNTTLQEGYASLDVKYPP--VIVEM 245
QY 188 SRDNTPALEPQGNVPLEAKQGFLLCAADSQPATLSVLQNRVLSHHPWGRPP 247
Db 246 NSS-----VEAIEGSHVSLLCGADSNPPPLLTWMDGMYLREA---VAES 287
QY 248 LGLELPGVKAGDSGRYTCRAENRLGSGQALDLSVQYPPENLRVNVMSQANRTVLENLGN 307
Db 288 LYLDEEVTPAEDGIYACLAENAYQDNRTVELSVMYAPWKPVT-----NG 333
QY 308 TSLPVLGQSLCLVCTVTHSSPPARLSWTQGVLSFSPQSDPGVLELPRVQVEHEGFTC 367
Db 334 TVAV-EGEVTSLGTSQSNPDPIITFKKQILATVYESQLQLELPAVTPDDGGEYWC 392
QY 368 HARHPLGSHVLSLSVHYSPKLLGPS-CSWEAEGHLCSCSQASPAPSLRWMLGEELE 426
Db 393 VAENQYQGRATAFNLSVFPAPILLESCHCAARDVQCLCVKSNPESVAFELPSRNV 452
QY 427 GNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEAWNVHGAQSGSIQLPKKGLI 486
Db 453 VNETEREF-VYSESGLLTSLTRGQAQAPPRVICTSRNLYGTQS---LPLP----- 502
QY 487 STAFSNG-----AFIGIGITALLFLCLALIMKILPKERTQTETPRPFS 531
Db 503 ---FOGAHRLMWAIGPVGAVFAILIAIVCYITQTRKKNVTSPSFS 549

RESULT 4

B33785
myelin-associated glycoprotein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 23-Jul-1999
C:Accession: B33785; A33785; S05687; S02374
R:Fujita, N.; Sato, S.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Inuzuka, T.; Takahashi, I
Biochem. Biophys. Res. Commun. 165, 1162-1169, 1989
A:Title: cDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splic
A:Reference number: A33785; MUID:90121220; PMID:2482022
A:Accession: B33785
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-637 <FUJ>
A:Cross-references: GB:M31811
A:Accession: A33785
A>Status: preliminary

J. Immunol. 141, 2797-2800, 1988
 A:Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid progenitor cells
 A:Reference number: A30521; MUID:89009814; PMID:3139766
 A:Accession: A30521
 A:Molecule type: mRNA
 A:Residues: 1-364 <SIM>
 A:Cross-references: UNIPROT:P20138
 C:Genetics:
 A:Gene: GDB:CD33
 A:Cross-references: GDB:119762; OMIM:159590
 A:Map position: 19q13.3-19q13.4
 C:Keywords: glycoprotein; surface antigen; transmembrane protein
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-259/Domain: extracellular #status predicted <EXT>
 F:260-282/Domain: transmembrane #status predicted <TM>
 F:283-364/Domain: intracellular #status predicted <CYT>
 F:100,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.4%; Score 451.5; DB 2; Length 364;
 Best Local Similarity 21.3%; Pred. No. 2.6e-22;
 Matches 148; Conservative 49; Mismatches 110; Indels 389; Gaps 11;

QY 1 MLLPULLSSLLGGQAMVGRFWRVQBSVMVPEGLCISVPCFSYPRQDWTGTPAYGYW 60
 DB 1 MPLLPLPALLMAGALAMPNFWLQVQBSVTVQEGLCVLPCTFPHPPIPYDYDKNSPVHGYW 60

QY 61 FKAVTETTKAPVATNHQSRSEVEMSTGRFQLTCDPAKGNCSLVIRDAQMDQESQYFVRV 120
 DB 61 FREGAIIISGSPVATNKLDOEVEETQGRFLLGDPGRNNCSLSIVDARRDNGSYFFRM 120

QY 121 ERGSYVAYNFMNDGFFLKVT 140
 DB 121 ERGS-TKSYKSPQLSVHVDLTHRPKILIPGLTLEPGHKNLTCYSWACEQGTPIFSW 179

QY 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRDLV 184
 DB 180 LSAAPTSLSGPRTHSSVLIITPRPDHNTLTCQVPAGAGVTTERTIQLNVTV 235

QY 185 ISISRDNTPALEPOQGNVPLEAQKQFLRLCAAQDOPATLSWVLQNRVLSHHPWG 244
 DB 236 -----NQPTT----- 240

QY 245 PRPLGLELPVQAGD-SGRYTCRAENRLGQQRALDLSVQYPPENLRVWVSQANRTVLEN 303
 DB 241 -----GTFPGDGSCKOETRA----- 255

QY 304 LGNCTSLPVLEGQSLCLVCTHSPPARLSMTQGVLSFSPQSDPGVLELPRVQVEHEG 363
 DB 256 -----GV----- 257

QY 364 EFTCHARHPLGSHVLSLSVSHYSPKILGSPCSWEAEGHLCSCSSQASPAFLRWMLGEE 423
 DB 258 -----VHGAIGGA----- 265

QY 484 GLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTETPRPRFSRHSITLDYINVV 543
 DB 266 -----GVTALLALCLCLIFIVKTHRKAARTAVGRNDTH----- 300

QY 544 PTAGPLAKKNQKATNSPRTPLPGAPSPESKKNOKKQVLPSPFPKSKSTQAPESQES 603
 DB 301 PTTGSASPKEKSKSLHGP-----TETSCSGAAPTIVEM 334

QY 604 QEELHVAATNLPVGRPEARMKPGTQADYAEVKFO 639
 DB 335 DEELHVASLNFHGNP-----SKDTSTEYSEVTRTQ 364

N:Alternate names: B-cell membrane protein CD22
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: JH0371; I56171
R:Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.
J. Exp. Med. 173, 137-146, 1991
A:Title: cDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell interaction
A:Reference number: JH0371; MUID:91086838; PMID:1985119
A:Accession: JH0371
A:Molecule type: mRNA
A:Residues: 1-847 <WILL>
A:Cross-references: UNIPROT:O60926; GB:X59350; NID:G36090; PIDN:CAA42006.1; PID:G36091
A:Experimental source: B lymphocyte
A:Note: the authors translated the codon AAT for residue 358 as Met
R:Wilson, G.L.; Naifeid, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.
J. Immunol. 150, 5013-5024, 1993
A:Title: Genomic structure and chromosomal mapping of the human CD22 gene.
A:Reference number: I56171; MUID:93267103; PMID:8496602
A:Accession: I56171
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 121-269, 'T', 271-473, 'K', 475-614, 'R', 616-638, 'Y', 640-711, 777-847 <WIL2>
A:Cross-references: GB:S61375; NID:G385980; PIDN:AAC18956.1; PID:G3184492
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
A:Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-847/Product: B lymphocyte cell adhesion protein #status predicted <MAT>
F:346-398/Domain: immunoglobulin homology <IMM1>
F:609-661/Domain: immunoglobulin homology <IMM2>
F:688-705/Domain: transmembrane #status predicted <TRA>
F:67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (covalent)
F:764,789/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 8.6%; Score 289.5; DB 2; Length 847;
Best Local Similarity 20.0%; Pred. No. 3.1e-11;
Matches 181; Conservative 116; Mismatches 278; Indels 331; Gaps 40;

QY 1 MLLPILLSLGGSGAMGRFWI-RVQSFVMVPEGLCISVPCSFSS-----YPRQ 48
DB 3 LLGPWLLLVLELAFSSSKWVFPETLYAWEGACVMIPTYPALDGDLESFILFNP 62
QY 49 DWTGTPAYGWFKAVTETTKGAPYATNHSREVMSTRGRFQLTGDPKAGNCSLVIRDA 108
DB 63 EYKNTSRFD--GTRLYESTKDGKVP-----SEQKRVQFLGDKNK-NCILSIHPV 109

QY 109 QMQDSQYFFRVER-----VTV-----LSFTPRPDHNTDLTCHV-DFSRKGV 166
DB 110 HLNDGQLGLRMESKTEKWMERIHLNVSRPPPHIQLPPETQESQEVTLTCLLNFSCYG 169

QY 124 SVRYNFNDGFLX-----VTV-----LSFTPRPDHNTDLTCHV-DFSRKGV 166
DB 170 YPIQLWLLGVPMQAAVTSLSIKSVFTSELSKFSQWGHGKIVTCQLQDADGKFL 229

QY 167 S-----AQTVRRLRVAYAPRDLVI-----SIIRD 190
DB 230 SNDTVQLNVKHPKLEIKVTPSDAIVREGDSVTMTCEVSSNPEVTVSWLKDGTSLKKQ 289

QY 191 NTPALE-----POPG-NVPYLEAQGGFL 214
DB 290 NTFTLNLREVTQDGGKYCCQVNDVGRSBEVFLQVYAFEPSTVQILHSPAVEGSOV 349

QY 215 RLICAADSP-PATLSWV-----LQNRVLSHHPGPRPLGLELVKAGDSGRYTCRAE 268
DB 350 EFLCNSLANPLTNTYTHNGKEMQGRTEKH-----IPKILFWHAGTVSCVAE 399

QY 269 NPLGSOQR--ALDLSVYPPENLRVWVSOANVTLENLNGTSLSPLVLEGSQSLVCVTHS 326
DB 400 NILGTQGRFGAELDYQYPPKKV-----TTVIQN-----PMPIREGDTVTLSCNYS 446

QY 327 SPFA--RLSWTQGVLSQSPQSDPGVILPRVQVHEGEFTCHARPLGSGHVSLSLV 384
DB 447 SNFSVTRYEKPHGAEPEPSL-----GVLIQNVGWDNT-TIACARCNWSWASPVALNV 501

QY 385 HYSF-----KLLGSPSCSWEAEGLHSCSSQASPAISRLRWMLGBELLEGNSSQDSFE- 435
DB 502 QYAPRDVRVRKIRPLSEIHSGNSVSLQCDPSS-SHPKEVQFFWEKNGRLLGKESQLNFD 560

QY 436 VTFSSAGP--WANSLS-----LHGLSSG-----LRLRCEA-- 465
DB 561 ISPEDAGSYSCWYNSIGQTASKAWLTLEVLYAPRLRVSNPGDQVMEGKSATLTCESDA 620

QY 466 -----WN-----VHGAQSGSILQLPDKK-----GLIS-----TA 489
DB 621 NPPVSHYTWFDWNNQLPHSQK---LRLEPVQVHSGAYWCQGTNSVGKGRSPLSTLT 677

QY 490 FSNAGFICIGITALFLCLALIMKI-----LPKR--RTQTET-----PPRFS 531
DB 678 YSPETIGRRVAVGLGSLAILILAILCGLKQRWKRTQSQGLQENSSQGSFFVRNKKV 737

QY 532 RHTSLIDYINVVPTAGLAQRNQAIPNSPRPLPPGAPSPESK----- 576
DB 738 RRAPLSEGGHSLGCVNPMEDGG:SYTTLRPFEMNIPRTGDAESSEMQRPRPTCDDTVTYS 797

QY 577 ---KNQKKQYQ--LPSFPPEPKSQTAPESQSEELHYATLNPFGVPRPEARMPKGTQA 631
DB 798 ALHKRQGVYENVIPDPFE-----DEGIHYSILQFGVGERPQAQ-----ENV 840

QY 632 DYAEVK 637
DB 841 DYVILK 846

RESULT 11
S50065
Sialoadhesin - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S50065
R:Crocker, P.R.; Mucklow, S.; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, S.; Milc
EMBO J. 13, 4490-4503, 1994
A:Title: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic cells
A:Reference number: S50065; MUID:9500950; PMID:7925291
A:Accession: S50065
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1694 <CRO>
A:Cross-references: UNIPROT:Q62230; EMBL:Z36293; NID:G557253; PIDN:CAA85290.1; PID:G55725

Query Match 8.4%; Score 282.5; DB 2; Length 1694;
Best Local Similarity 22.0%; Pred. No. 2.2e-10;
Matches 135; Conservative 71; Mismatches 199; Indels 209; Gaps 21;

QY 5 LLLSLGGSGQMDGRFWRVQSFVMVPEGLCISVPCSFSPQDWTGTSPAYGWFKAV 64
DB 8 LLLASVSLQTTWG---VSSPNVQGLSGCLLICIFISYP-ADVPVNGITAIWY--Y 61

QY 65 TETTKGAPATNHSREVMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS 124
DB 62 DYSGKRWIHSQDPKLVDRKFRGRAELMGMDHKVKNLLKDLKPEDSGTYNFRFEISD 121

QY 125 YVRNFMNDGFFLKVTVLSTPRP----- 148
DB 122 SNRW-----LDVKGTITVTITDPSPTTIPPELRGEMERNFNCSTPYCLCEKQVSLQ 175

QY 149 -----QDHTDLTCHVDFSRKGVSAQRTVRL 174
DB 176 WRGQDPHTSVTSFQSLPTGYSYHQTTLHMAWSQDGHGRTLLC--QPSLGHSSRKEVYL 233

QY 175 RVAYAPRDLVISIRNDNTPALEFQP-----QGVNPLYEAQK-----GQFLR- 215
DB 234 QVHPAPKGVLEILLSGSGNRLPGDPVTLTCRVNSSYPVAVSQAOWARDGVNLGVTGHVRL 293


```
Db 3398 SPTPTQV-----TPQLETKSIGASVEFHCAPVSDGTLRFKEGGQLPPCHSVQDGVLR 3452
QY 354 LRVQVEHEGFTCHARPLGSGHVSLSLHYSPKLL-----GPGSCSWAEG 401
Db 3453 IQNLDQSCQGYICQAHGFWKQAQSLVQALPSVLINTRTSYQTVVGHAVEFE--- 3509
QY 402 LHCSCSSQASPAFSLRWLGEELLEGNSQDSFEVTPSSAGFWANSSLSLHGG----- 454
Db 3510 ----CLAGDQXPQVW-----SKVGHLPFGIVQSGGVVRIAHV 3545
QY 455 -LSSGLRLRCERANVHGAQSSILQLPDKKGLISTAFNGAFLGIGITALLFLCLA 509
Db 3546 ELADAGVRCATNAAGTTQSHVLLVQALPQISMPOEVRVPAG---SAAVFPCTA 3598

RESULT 13
138000
Lutheran blood group glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38000; S51663
R:Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.; Mawby, W.J.
Proc. Natl. Acad. Sci. U.S.A. 92, 5496-5500, 1995
A:Title: The Lutheran blood group glycoprotein, another member of the immunoglobulin sup
A:Reference number: I38000; MUID:95296337; PMID:7777537
A:Accession: I38000
A:Molecule type: mRNA
A:Residues: 1-628 <RES>
A:Cross-references: UNIPROT:P50895; EMBL:X83425; NID:G603559; PIDN:CAA58449.1; PID:G6035
A:Note: parts of this sequence, including the amino end of the mature form, were confirm
C:Genetics:
A:Gene: GDB:IJ
A:Cross-references: GDB:120155; OMIM:111200
A:Map position: 19c12-19q13
C:Keywords: glycoprotein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-628/Product: Lutheran blood group glycoprotein #status experimental <MAT>

Query Match 7.4%; Score 251.5; DB 2; Length 628;
Best Local Similarity 23.3%; Pred. No. 6.7e-09;
Matches 162; Conservative 79; Mismatches 231; Indels 223; Gaps 40;

QY 5 LILSSLLGSSQAMDGFWIRVQESVWVPEGLCISVPCSFSPRODWTGSTPAYGY-WFKA 63
Db 17 LLLAVLLAAHPDAQAEVRLSVPLVEMVRGKSVILDCT---P---TGDHMYLWEP-- 67
QY 64 VTETTKGAP--VATNHQSEVMS---TRGR---FQLTGDPKAGNCSLVIRDAQMDQDSQ 115
Db 68 LIDRSQARPLASAEWQSGELOVTHDTRGSPFPQL---DSQGR--LVLAQAQVGDDEED 122
QY 116 YFRRVERG-----SYVRVNF----- 130
Db 123 YVWVRAGAAGTAETARLNVFAKPEATEVSPNKGTLVWSDSAQEIATCNSRNGNPAPK 182
QY 131 -----MN-DGFFLKVTV-----LSFTP-----RPQDHTDLTCHVDPS 162
Db 183 ITWYRNGQLEVPVENPGEYTSRTVREASGLLSLTSTLYLRKDRDASFHCAHYIS 242
QY 163 ----RKGVSQARTVRLVAYAPRDLVISRDNTPALEPQPGNVPYLEAQKGQFLRLLC 218
Db 243 LPEGRHRLDSPTFHLTLHPTEHVQFWGSPSTPA-----GWV-----REGDTVQLLC 291
QY 219 AADSQP-PATLSWLQN-----RVLSSSHPPGPRPLGLLELPCVKAGDSGRVTCBAENELQSQ 274
Db 292 RGDGSPSPYTLFRQLQDEQEEVLNVLEG-----NLTEGVTRGOSGTYGCRVEDYDAAD 346
QY 275 ----QALDLSVQY---PPENLRVWVMSQANRTVLENLNGTSLPVLGOSLCLVCVTHSSP 328
Db 347 DVQLSKTLRLVAYLDPLE-----LSEKVLSLPLNSAVVNCVHGGLP 390
QY 329 PARLSWTQRQGVLSPSQSDPGVLELPRVQVHEGEFTCHA---RHPLGSGHVSLSLSVH 385
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Db 391 TPALRWTKDSTPL-----GDGPMLSSITFDNGTYVCEASLPTVPVLSRTQNTLLVQ 445
QY 386 YSPKL-----LGPSC--SW-EAEGLHCSCSSQASPAFSLRWLGEELLEGNSQDSPEVTP 438
Db 446 GSELKTAETEPKADGSGWREGDEVTLICARGHPDKLSW-----SQLGSGPA-----EPIP 497
QY 439 SSAGPWANSSLSLHGLSSGLR---LRCEAWNVHGAQS-----GSILQLPDKKG--LIST 488
Db 498 GRQG-WYSSSLTLK--VTSALSRDGISCEASNPNGNKRHVFEFGAVSPQTSQAGVAMAV 554
QY 489 AFNGAFLGIGITALLFLCLALIMKILPKRQTQETPRPFRSHRTILDYINVVTAGP 548
Db 555 AVSVGLLL---LVVAVFYCV-----RR-----KGGP 577
QY 549 LAQRNOKATPNSPRTPLPFGAPS-PESKKNQKKQ 582
Db 578 CCRQRREKAP-----PGEFGLSHSGSEQPEQ 605

RESULT 14
A35648
B-cell adhesion protein CD22 alpha splice form precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 15-Mar-2004
C:Accession: A35648
R:Stamenkovic, I.; Seed, B.
Nature 345, 74-77, 1990
A:Title: The B-cell antigen CD22 mediates monocyte and erythrocyte adhesion.
A:Reference number: A35648; MUID:90231465; PMID:1691828
A:Accession: A35648
A:Molecule type: mRNA
A:Residues: 1-647 <STA>
A:Cross-references: GDB:X52785; NID:G29778; PIDN:CAA36988.1; PID:G29779
C:Genetics:
A:Gene: GDB:CD22
A:Cross-references: GDB:127545; OMIM:107266
A:Map position: 19q13.1-19q13.1
C:Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; transmembr
F:1-19/Domain: signal sequence #status predicted <EXT>
F:20-510/Domain: extracellular #status predicted <EXT>
F:432-484/Domain: immunoglobulin homology <IMM>
F:511-529/Domain: transmembrane #status predicted <TM>
F:530-647/Domain: intracellular #status predicted <CYT>
F:67,101,112,135,164,231,268,302,397,457/Binding site: carbohydrate (Asn) (covalent) #sta

Query Match 7.3%; Score 245; DB 2; Length 647;
Best Local Similarity 21.9%; Pred. No. 1.9e-08;
Matches 133; Conservative 72; Mismatches 197; Indels 206; Gaps 26;

QY 1 MLLPLLLSSLLGGSQAMDGFWI-RVQESVWVPEGLCISVPCSFSP-----YPRQ 48
Db 3 LLGFWLLLLVLYLAFSDSSKNVFEHPETLYANEGACVWIPCTYRALDGDLESPILFHP 62
QY 49 DWTGSTPAYGYWFKAVTETTKGAPVATNHQSEVMSRTRGFLTGDPKAGNCSLVIRDA 108
Db 63 EYNKNTSKFD--GTRLYESTKDGKVP-----SEKRVQFLGDKNK-NCTLSHPV 109
QY 109 QMDESQYFRVER----- 123
Db 110 HLNDSSGQLGRMESKTEKMERIHLNVSRPPPHIQLPEIQESQVTLTCLLNFSCYG 169
QY 124 SYVRVFNMDGFFLK-----VTV-----LSFTPRPDHNTDLTCHVDFSRKGS 167
Db 170 YPIQLQMLLEGVPMRQAATVSTLSIKSVTRSELKPSQWSSHGKIVTCQLQADGKFL 229
QY 168 AQRVTRVRLVAYAPRDLVISI-----SRDNTPALEPQPGQ--NVPI 205
Db 230 SNTDVQNVKHPKKVTVI-QNMPPIREGDVTILSCNYSNPSVTRYEMKPHGAWPEPS 289
QY 206 LEAQKGQFL-----RLCAADSOPPALTSWLQN-----RV----- 236
Db 290 LVVLKIQNVGWDNTIACACNSWCSNAPVALNVQAPDRVRKIKELPSLSEIHSGNSVS 349
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QY 237 -----LSSHP-----W--GPRPLG-----LELPVWAGDSGRYTCRAENRLG-SQORALD 279
DB 350 LQDFSSHPKEVQFFWEXNGRLLGKESQINFDSISPEDAGSYSCWVWNSIGQTASKAWT 409
QY 280 LSVQYPPENLRVMVSOANRTVLNGLNGTSLPVLQGSCLVCVTHSSPPAR-----LSWT 335
DB 410 LEVLYAPRRLRVMSKSPCDQ-----VWEGKSATLICESDANFPVSHYTFWFDN 456
QY 336 QROQVLSPOQSPDPGVLELRVQVEHEGFTCHARHPLGSHQVLSL-LSVHYSPLKLGES 394
DB 457 NQ-----SLPYHSQKRLLEPVVQVHSGAYWCGTNSVGKRSPLSLTVVYSPETIGR 510
QY 395 CSWEAEGH-----CSCSSQASAPSLRW--WLGEELLEGSSQDSFEV-----436
DB 511 V-----AVGLSGSLAILILA:CGKLQR-----RWKRTSQOGLQENSSGQSFFVRNKKVR 561
QY 437 -TPSSAGP 443
DB 562 RAPLSEGP 569

RESULT 15
137202
B-CAM protein - human
C:Species: Homo sapiens (man)
G:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
W:Accession: I37202; S47272
R:Campbell, I.G.; Foulkes, W.D.; Senger, G.; Trowsdale, J.; Garin-Chesa, P.; Rettig, W.J.
Cancer Res. 54, 5761-5765, 1994
A:Title: Molecular cloning of the B-CAM cell surface glycoprotein of epithelial cancers:
A:Reference number: I37202; PMID:95042237; PMID:7954395
A:Accession: I37202
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-588 <RES>
A:Cross-references: UNIPROT:P50895; EMBL:X80026; NID:G535178; PIDN:CAAS6327.1; PID:G5351
C:Genetics:
A:Gene: B-CAM

Query Match 7.1%; Score 239.5; DB 2; Length 588;
Best Local Similarity 23.1%; Pred. No. 3.8e-08;
Matches 155; Conservative 78; Mismatches 223; Indels 215; Gaps 38;

QY 5 LLSLSLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSFSPYRQDWTGTSTPAYGY-WFKA 63
DB 17 LLLAVLLAAHPDAQAEVRLSVPLVWEGSKVILDCT---P-----TGTHDHYMLEWF-- 67
QY 64 VTETTKGAP--VATNHQSEVMS---TRGR---PQLTGDPAKGNCSLVIRDAQMQDESQ 115
DB 68 LTDRSGARPLASAEWQSGSELOQVTHDTRGRSPPYQL---DSQGR--LVLAEAQVGDGRD 122
QY 116 YFFRVERG-----SYVRYNF-----130
DB 123 YVCVVRAGAGTAETARLNVFAKPEATEVSFNKGTLSVMEDSAQEIATCNRSNGNPAPK 182
QY 131 -----MN-DGFFLKVTV-----LSFTP-----RPQHNITDLTCHVDPS 162
DB 183 ITWYRNGRLEVPVEMNPEGYMSTRVREASGLLSLSTLYLPCRKDRDASFHCAAHYS 242
QY 163 ----RKGVSQAQTVRLVAVAPRDLVIS:SRONTFALEPQPOGNNVYLEAKQGQFLRLIC 218
DB 243 LPEGRHRLDSTFHLTHLYPTEHVQVWGSPTFA-----GWV-----REGDTVQLLC 291
QY 219 AADSQP-PATLSWLNQ-----RVLSSSHFMGPRPLGLELPGVKAGDSGRYTCRAENRLG 274
DB 292 RGDGSPSPVYTLFRLQDEQEVLNVNLEG-----NLTEGVTRGQSGTYGCKVEDYDAAD 346
QY 275 ----QKALDSVQY--PPENLRVMVSOANRTVLNGLNGTSLPVLQGSCLVCVTHSSP 328
DB 347 DVQLGKTLDRVAYLDPLE-----LSEGKVLSTPLNNSAVVNCVSHGLP 390
QY 329 PARLSWTQRGOVLSQSPQDPGVLELRVQVEHEGFTCHA---RHLPGSQHVSLSLVH 385
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DB 391 TPALRWTKDSTPL-----GDGFMLSLSSITFDNGTIVVCEASLFTVPVLSTQNFLLVQ 445
QY 386 YSPKL-----LQPSG--SW-EAEGHLHCSSQASAPSLRWMLGEELEGNSSQDSFEVTP 438
DB 446 GSPELKTAETPRKADGWSREGDEVTLICSAARGHPDPKLSW---SQLGGSPA-----EPIP 497
QY 439 SSAGPWANSSLSLHGGLSGSLR---LRCEANNVHGAQS-----GSLIQLPDKKG--LIST 488
DB 498 GRQG-WYSSSLTLK--VTSALSRDGISCEASNPHGNKRHVHFHGAVSPQTSQAGVAVNAV 554
QY 489 AFSNGAFLGIGITALLFLCLALIMKILPKRRTQTETPRPRFSRHSHTILDYINNVPTAGP 548
DB 555 AVSVGLLL---LVAVFYCV-----RR-----KGGP 577
QY 549 LAQFRNOKATP 559
DB 578 CCQRQREKGP 588
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Search completed: November 5, 2004, 13:51:06
Job time : 22.76s4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:53:32 ; Search time 109.924 Seconds
(without alignments)
2053.348 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377
Sequence: 1 MLLPILLSLLGGSQAMDGR.....RPEARMPKGTQDYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubpaa/FCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
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- 9: /cgn2_6/prodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3377	100.0	639	14	US-10-158-238-28
2	3354	99.3	639	10	US-09-984-130-33
3	3354	99.3	639	10	US-09-836-353A-33
4	3338	98.8	697	10	US-09-910-600-28
5	3334	98.7	697	10	US-09-984-130-149
6	3334	98.7	697	15	US-10-403-938-7
7	3334	98.7	697	16	US-10-614-853-10
8	3299	97.7	622	10	US-09-910-600-9
9	2803.5	83.0	544	10	US-09-910-600-8
10	2790.5	82.6	544	9	US-09-978-295A-259
11	2790.5	82.6	544	9	US-09-978-697-259
12	2790.5	82.6	544	9	US-09-978-192A-259
13	2790.5	82.6	544	9	US-09-999-832A-259

14	2790.5	82.6	544	10	US-09-978-189-259	Sequence 259, App
15	2790.5	82.6	544	10	US-09-978-608A-259	Sequence 259, App
16	2790.5	82.6	544	10	US-09-978-585A-259	Sequence 259, App
17	2790.5	82.6	544	10	US-09-978-191A-259	Sequence 259, App
18	2790.5	82.6	544	10	US-09-978-403A-259	Sequence 259, App
19	2790.5	82.6	544	10	US-09-978-564A-259	Sequence 259, App
20	2790.5	82.6	544	10	US-09-999-833A-259	Sequence 259, App
21	2790.5	82.6	544	10	US-09-981-915A-259	Sequence 259, App
22	2790.5	82.6	544	10	US-09-978-824-259	Sequence 259, App
23	2790.5	82.6	544	10	US-09-918-585A-259	Sequence 259, App
24	2790.5	82.6	544	10	US-09-999-834A-259	Sequence 259, App
25	2790.5	82.6	544	10	US-09-978-423A-259	Sequence 259, App
26	2790.5	82.6	544	10	US-09-978-193A-259	Sequence 259, App
27	2790.5	82.6	544	10	US-09-999-830A-259	Sequence 259, App
28	2790.5	82.6	544	10	US-09-978-757A-259	Sequence 259, App
29	2790.5	82.6	544	10	US-09-978-187B-259	Sequence 259, App
30	2790.5	82.6	544	10	US-09-978-643A-259	Sequence 259, App
31	2790.5	82.6	544	10	US-09-978-375A-259	Sequence 259, App
32	2790.5	82.6	544	10	US-09-978-298A-259	Sequence 259, App
33	2790.5	82.6	544	10	US-09-978-188A-259	Sequence 259, App
34	2790.5	82.6	544	10	US-09-978-681A-259	Sequence 259, App
35	2790.5	82.6	544	10	US-09-978-194A-259	Sequence 259, App
36	2790.5	82.6	544	10	US-09-999-829A-259	Sequence 259, App
37	2790.5	82.6	544	10	US-09-978-299A-259	Sequence 259, App
38	2790.5	82.6	544	10	US-09-978-544A-259	Sequence 259, App
39	2790.5	82.6	544	10	US-09-978-665A-259	Sequence 259, App
40	2790.5	82.6	544	10	US-09-978-802A-259	Sequence 259, App
41	2790.5	82.6	544	11	US-09-999-831A-259	Sequence 259, App
42	2790.5	82.6	544	13	US-10-052-586-118	Sequence 118, App
43	2790.5	82.6	544	14	US-10-174-590-118	Sequence 118, App
44	2790.5	82.6	544	14	US-10-176-758-118	Sequence 118, App
45	2790.5	82.6	544	14	US-10-175-737-118	Sequence 118, App

ALIGNMENTS

RESULT 1

US-10-158-238-28
; Sequence 28, Application US/10158238
; Publication No. US20030040604A1
; GENERAL INFORMATION:
; APPLICANT: Immurex Corporation
; APPLICANT: Dirk, Anderson M.
; APPLICANT: Maken, John S.
; TITLE OF INVENTION: SIGLEC-12 POLYPEPTIDES, POLYNUCLEOTIDES, AND METHODS OF USE THEREC
; FILE REFERENCE: 3290-A
; CURRENT APPLICATION NUMBER: US/10/158,238
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/294,199
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 28
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-158-238-28

Query Match 100.0%; Score 3377; DB 14; Length 639;

Best Local Similarity 100.0%; Pred. No. 2e-221;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLLPILLSLLGGSQAMDGRFWIRVQSVVMVPEGLCI:SVPCSFSPYPRQDWTGSTPAYGYW	60
Db	1	MLLPILLSLLGGSQAMDGRFWIRVQSVVMVPEGLCI:SVPCSFSPYPRQDWTGSTPAYGYW	60
Qy	61	FKAVTTTKGAPVATNHQSRREVSTGRFOLTGDPAKNCSLVIRDAQMDQSYFFRV	120
Db	61	FKAVTTTKGAPVATNHQSRREVSTGRFOLTGDPAKNCSLVIRDAQMDQSYFFRV	120
Qy	121	ERGSVRYNFNDGFFLKVTVLSTPDPDHTDLTCHVDFSRKGVSAQRTVRLRVAYAP	180

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241 HPWGPRLGLELPGVAKGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSOANRTV 300
301 LENLNGTSLPVLGGQSLCLVCTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVE 360
301 LENLNGTSLPVLGGQSLCLVCTHSSPPARLSWTORGQVLSFSPQSDPGVLELPRVQVE 360
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421 GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEANVHGAQSGSLQLP 480
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481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPRFSRHSITLDYI 540
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601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639

RESULT 2

US-09-984-130-33
; Sequence 33, Application US/09984130
; Publication No. US2003005231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF4892
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-33

Query Match 99.3%; Score 3354; DB 10; Length 639;
Best Local Similarity 99.5%; Pred. No. 7.5e-220;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDCGFWRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DB 1 MLLPILLSLLGSGQAMDCGFWRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120

61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
121 ERGSYVRYNFMNDGFFLKVTVLSTFTPRPDHNTDLTCHVDFFSRKGVSAQRTVLRVAYAP 180
121 ERGSYVRYNFMNDGFFLKVTVLSTFTPRPDHNTDLTCHVDFFSRKGVSAQRTVLRVAYAP 180
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181 RDLVISISRDNTPALBPQGNVPYLEAQKGFRLRLCAADSPATLSSWLQNRVLSSS 240
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241 HPWGPRLGLELPGVAKGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSOANRTV 300
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541 NVVPTAGPLAQRNOKATPNSPRTPPPGAPSPESKKNQKQYQLPSPFPKPSSTQAPES 600
541 NVVPTAGPLAQRNOKATPNSPRTPPPGAPSPESKKNQKQYQLPSPFPKPSSTQAPES 600
601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639

RESULT 3

US-09-836-353A-33
; Sequence 33, Application US/09836353A
; Publication No. US20030129685A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF4892
; CURRENT APPLICATION NUMBER: US/09/836,353A
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-353A-33

Query Match 99.3%; Score 3354; DB 10; Length 639;
Best Local Similarity 99.5%; Pred. No. 7.5e-220;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDCGFWRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DB 1 MLLPILLSLLGSGQAMDCGFWRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120

61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
121 ERGSYVRNFMNDGFFLKVTLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 180
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241 HPWGRPLGLELPYGKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVSOANRTV 300
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301 LENLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGQVLSPPSPDPGVLELPRVQVE 360
301 LENLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGQVLSPPSPDPGVLELPRVQVE 360
361 HGEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGHLCSSQASPAFLRWL 420
361 HGEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGHLCSSQASPAFLRWL 420
421 GEELEGNSSQDSFEVTPSSAGFWANSSLSLHGGSSGLRLRCEAWNVHGAQSGSILQLP 480
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481 DKKGLISTAFNGAFIGITALLFLCLALIIIMKILPKRRTOTETPRFRSHSTILDYI 540
481 DKKGLISTAFNGAFIGITALLFLCLALIIIMKILPKRRTOTETPRFRSHSTILDYI 540
541 NVVPTAGPLAQRNOKATPNSPRTPLPGAPSPESKQKQYQYLPSPFPKSSSTQAPES 600
541 NVVPTAGPLAQRNOKATPNSPRTPLPGAPSPESKQKQYQYLPSPFPKSSSTQAPES 600
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RESULT 4
US-09-910-600-28
; Sequence 28, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/220,139
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L3-995-2
US-09-910-600-28
Query Match 98.8%; Score 3338; DB 10; Length 697;
Best Local Similarity 91.7%; Pred. No. 1e-218;
Matches 639; Conservative 0; Mismatches 0; Indels 58; Gaps 1;
QY 1 MLPLLLSLLGGSQAMDRFIRVOESVMPVEGLCISVPCSFSPYPRQDWTGSTPAYGW 60
DB 1 MLPLLLSLLGGSQAMDRFIRVOESVMPVEGLCISVPCSFSPYPRQDWTGSTPAYGW 60
QY 61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120

61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
121 ERGSYVRNFMNDGFFLKVTLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 140
121 ERGSYVRNFMNDGFFLKVTLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 180
141 -----VLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 182
181 TGAALSSQGTPTTSHFSVLSFTPRQDHNHDTLCHVDFSRKGVSAQRTVRLVAYAP 240
183 LVISISRDNTPALEPOQGNVPYLEAKGQFLRLCAADSOPPATLSWLQNRVLSSSHP 242
241 LVISISRDNTPALEPOQGNVPYLEAKGQFLRLCAADSOPPATLSWLQNRVLSSSHP 300
243 WGRPRPLGLELPYGKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVSOANRTVLE 302
301 WGRPRPLGLELPYGKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVSOANRTVLE 360
303 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGQVLSPPSPDPGVLELPRVQVEHE 362
361 NLNGTSLPVLGOSLCLVCTHSSPPARLSWTQRGQVLSPPSPDPGVLELPRVQVEHE 420
363 GEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGHLCSSQASPAFLRWLGE 422
421 GEFTCHARHPLGSHQVLSLSVHYSPKLLGSPCSWEAEGHLCSSQASPAFLRWLGE 480
423 ELLEGNSSQDSFEVTPSSAGFWANSSLSLHGGSSGLRLRCEAWNVHGAQSGSILQLPDK 482
481 ELLEGNSSQDSFEVTPSSAGFWANSSLSLHGGSSGLRLRCEAWNVHGAQSGSILQLPDK 540
483 KGLISTAFNGAFIGITALLFLCLALIIIMKILPKRRTOTETPRFRSHSTILDYINV 542
541 KGLISTAFNGAFIGITALLFLCLALIIIMKILPKRRTOTETPRFRSHSTILDYINV 600
543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKQKQYQYLPSPFPKSSSTQAPESQ 602
601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKQKQYQYLPSPFPKSSSTQAPESQ 660
603 SQEELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
661 SQEELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 697

RESULT 5
US-09-984-130-149
; Sequence 149, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489F2
; CURRENT APPLICATION NUMBER: US/09/984,130
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 149
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-130-149
Query Match 98.7%; Score 3334; DB 10; Length 697;
Best Local Similarity 91.5%; Pred. No. 1.9e-218;

Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MLLPILLSLLGGSQAMDRFWIRVQESVMVPEGLCISVPCFSFYPRQDWTGTTPAYGYW 60
 DB 1 MLLPILLSLLGGSQAMDRFWIRVQESVMVPEGLCISVPCFSFYPRQDWTGTTPAYGYW 60

QY 61 FKAVTETTKGAPVATNHQSEVENSTGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
 DB 61 FKAVTETTKGAPVATNHQSEVENSTGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120

QY 121 ERGSYVRYNFMNDGFFLKVT----- 140
 DB 121 ERGSYVRYNFMNDGFFLKVTALTKPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSW 180

QY 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 182
 DB 181 TGAALSSQGTKPTTSHFVSLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 240

QY 183 LVISISRDNTPALEPOQGNVPYLEAQKQFLRLCAADSQPPATLSWLQNRVLSSSH 242
 DB 241 LVISISRDNTPALEPOQGNVPYLEAQKQFLRLCAADSQPPATLSWLQNRVLSSSH 300

QY 243 WGRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVQANRTVLE 302
 DB 301 WGRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVQANRTVLE 360

QY 303 NLGNGTSLPVLEQSLCLVCVTHSSPPARLSWTORGQVLSPOSPDPGVLELPRVQVEHE 362
 DB 361 NLGNGTSLPVLEQSLCLVCVTHSSPPARLSWTORGQVLSPOSPDPGVLELPRVQVEHE 420

QY 363 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEGLHCSCSQASPAAPSLRWMLGE 422
 DB 421 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEGLHCSCSQASPAAPSLRWMLGE 480

QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGSLGRLRCEAMNVHGAQSGSILQLPDK 482
 DB 481 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGSLGRLRCEAMNVHGAQSGSILQLPDK 540

QY 483 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 542
 DB 541 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 600

QY 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQ 602
 DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQ 660

QY 603 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 639
 DB 661 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 697

RESULT 6

US-10-403-938-7
 Sequence 7, Application US/10403938
 Publication No. US20040025195A1
 GENERAL INFORMATION:
 APPLICANT: Bristol-Myers Squibb Company
 TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,
 TYPE: PRT
 FILE REFERENCE: D0227 NP
 CURRENT APPLICATION NUMBER: US/10/403,938
 PRIOR FILING DATE: 2003-03-28
 PRIOR APPLICATION NUMBER: U.S. 60/368,422
 PRIOR FILING DATE: 2002-03-28
 NUMBER OF SEQ ID NOS: 88
 SOFTWARE: Patent in version 3.2
 SEQ ID NO 7
 LENGTH: 697
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-403-938-7

Query Match

98.7%; Score 3334; DB 15; Length 697;

Best Local Similarity 91.5%; Pred. No. 1.9e-218;
 Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MLLPILLSLLGGSQAMDRFWIRVQESVMVPEGLCISVPCFSFYPRQDWTGTTPAYGYW 60
 DB 1 MLLPILLSLLGGSQAMDRFWIRVQESVMVPEGLCISVPCFSFYPRQDWTGTTPAYGYW 60

QY 61 FKAVTETTKGAPVATNHQSEVENSTGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
 DB 61 FKAVTETTKGAPVATNHQSEVENSTGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120

QY 121 ERGSYVRYNFMNDGFFLKVT----- 140
 DB 121 ERGSYVRYNFMNDGFFLKVTALTKPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSW 180

QY 141 -----VLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 182
 DB 181 TGAALSSQGTKPTTSHFVSLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAPRD 240

QY 183 LVISISRDNTPALEPOQGNVPYLEAQKQFLRLCAADSQPPATLSWLQNRVLSSSH 242
 DB 241 LVISISRDNTPALEPOQGNVPYLEAQKQFLRLCAADSQPPATLSWLQNRVLSSSH 300

QY 243 WGRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVQANRTVLE 302
 DB 301 WGRPLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVQANRTVLE 360

QY 303 NLGNGTSLPVLEQSLCLVCVTHSSPPARLSWTORGQVLSPOSPDPGVLELPRVQVEHE 362
 DB 361 NLGNGTSLPVLEQSLCLVCVTHSSPPARLSWTORGQVLSPOSPDPGVLELPRVQVEHE 420

QY 363 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEGLHCSCSQASPAAPSLRWMLGE 422
 DB 421 GEFTCHARHPLGSHVLSLSVHSPKLLGPCSWAEGLHCSCSQASPAAPSLRWMLGE 480

QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGSLGRLRCEAMNVHGAQSGSILQLPDK 482
 DB 481 ELLEGNSQDSFEVTPSSAGPWANSSLSHGGSLGRLRCEAMNVHGAQSGSILQLPDK 540

QY 483 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 542
 DB 541 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYINV 600

QY 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQ 602
 DB 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSTQAPESQ 660

QY 603 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 639
 DB 661 SQBELHYATLNFPGVRPEARMKGTQADYAEVKFQ 697

RESULT 7

US-10-614-853-10
 Sequence 10, Application US/10614853
 Publication No. US20040138114A1
 GENERAL INFORMATION:
 APPLICANT: HILARY CHIU
 APPLICANT: HILARY CLARK
 APPLICANT: KATHRYN DENNIS
 APPLICANT: SHERMAN FONG
 APPLICANT: JILL SCHOENFELD
 APPLICANT: WILLIAM WOOD
 APPLICANT: THOMAS WU
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE
 TITLE OF INVENTION: RELATED DISEASES
 FILE REFERENCE: P197331-US
 CURRENT APPLICATION NUMBER: US/10/614,853
 PRIOR FILING DATE: 2003-07-08
 PRIOR APPLICATION NUMBER: US 60/394,485
 PRIOR FILING DATE: 2002-07-08
 NUMBER OF SEQ ID NOS: 28
 SEQ ID NO 10

```
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-614-853-10

Query Match      98.7%; Score 3334; DB 16; Length 697;
Best Local Similarity 91.5%; Pred. No. 1.9e-218;
Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

Qy 1 MLLPILLSLLGSGQAMGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
Db 1 MLLPILLSLLGSGQAMGRFIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
Qy 61 FRAVTTETTKGAPVATNHOSREVEVEMTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
Db 61 FRAVTTETTKGAPVATNHOSREVEVEMTRGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRV 120
Qy 121 ERGSVYRVNFMNDGFLKVT----- 140
Db 121 ERGSVYRVNFMNDGFLKVTALQKPDVVIPTLEPGQPVTVICVFNWAFECPPPSFW 180
Qy 141 -----VLSTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 182
Db 181 TGAALSSQGTKEPTTSHFVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRD 240
Qy 183 LVISISRDNTPALEPOQGNVPLYEAQKQOFLRLCAADSQPPATLSWVLQNRVLSSSH 242
Db 241 LVISISRDNTPALEPOQGNVPLYEAQKQOFLRLCAADSQPPATLSWVLQNRVLSSSH 300
Qy 243 WGPRLPLGLELPGVKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE 302
Db 301 WGPRLPLGLELPGVKAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE 360
Qy 303 NLNGTSLPLVEQSLCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHE 362
Db 361 NLNGTSLPLVEQSLCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHE 420
Qy 363 GFPTCHARPLGSOHVLSLSVHYSPKILGPCSWEAEGHLCSCSSQASPSLRWLWGE 422
Db 421 GFPTCHARPLGSOHVLSLSVHYSPKILGPCSWEAEGHLCSCSSQASPSLRWLWGE 480
Qy 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDK 482
Db 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDK 540
Qy 483 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTOTETPRFRSRHSTILDYINV 542
Db 541 KGLISTAFSNGAFLGIGITALLFLCLALIMKILPKRRTOTETPRFRSRHSTILDYINV 600
Qy 543 VPTAGPLAOKRQKATPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQ 602
Db 601 VPTAGPLAOKRQKATPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQ 660
Qy 603 SOBELHYATLNFPGVPRPEARMKPGTQADYAEVKFQ 639
Db 661 SOBELHYATLNFPGVPRPEARMKPGTQADYAEVKFQ 697

RESULT 8
US-09-910-600-9
; Sequence 9, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; PRIOR APPLICATION NUMBER: 60/220,139
; CURRENT FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32

Query Match      97.7%; Score 3299; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 4e-216;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 DGRFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYWFKAVTETTKGAPVATNH 77
Db 1 DGRFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYWFKAVTETTKGAPVATNH 60
Qy 78 QSREVENSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVVERGSYVRYNFMNDGFFL 137
Db 61 QSREVENSTGRFQLTGDPKAGNCSLVIRDAQMDQESQYFFRVVERGSYVRYNFMNDGFFL 120
Qy 138 KTVVLSSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRDVVISRDNTPALEP 197
Db 121 KTVVLSSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRAYAPRDVVISRDNTPALEP 180
Qy 198 QPQGNVPLYEAQKQOFLRLCAADSQPPATLSWVLQNRVLSSSHHPGPRPLGLELPGVKA 257
Db 181 QPQGNVPLYEAQKQOFLRLCAADSQPPATLSWVLQNRVLSSSHHPGPRPLGLELPGVKA 240
Qy 258 GDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLENLGNTSLPLVEGQS 317
Db 241 GDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLENLGNTSLPLVEGQS 300
Qy 318 LCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHEGEFTCHARHPLGSOH 377
Db 301 LCLVCVTHSSPPARLSWTORGQVLSPPQSDPGVLELPRVQVEHEGEFTCHARHPLGSOH 360
Qy 378 VLSLSVHYSPKILGPCSWEAEGHLCSCSSQASPSLRWLWGEELLEGNSQDSFEVT 437
Db 361 VLSLSVHYSPKILGPCSWEAEGHLCSCSSQASPSLRWLWGEELLEGNSQDSFEVT 420
Qy 438 PSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDKKGLISTAFSNGAFLG 497
Db 421 PSSAGPWANSSLSLHGGLSGRLRCEAMNVHGAQSGSILQLPDKKGLISTAFSNGAFLG 480
Qy 498 IGITALLFLCLALIMKILPKRRTOTETPRFRSRHSTILDYINVVPTAGPLAOKRQKA 557
Db 481 IGITALLFLCLALIMKILPKRRTOTETPRFRSRHSTILDYINVVPTAGPLAOKRQKA 540
Qy 558 TPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQESOEELHYATLNFPGV 617
Db 541 TPNSPRTPLPAGAPSPESKKNQKQYQLPSFPPEKSTQAPESQESOEELHYATLNFPGV 600
Qy 618 RPRPEARMKPGTQADYAEVKFQ 639
Db 601 RPRPEARMKPGTQADYAEVKFQ 622

RESULT 9
US-09-910-600-8
; Sequence 8, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
; APPLICANT: Longphre, Malinda
; APPLICANT: Chang, Han
; APPLICANT: Whitney, Gena
; TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
; FILE REFERENCE: D0003NP
; CURRENT APPLICATION NUMBER: US/09/910,600
; PRIOR APPLICATION NUMBER: 2001-07-20
; CURRENT FILING DATE: 2001-07-20
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
```

LENGTH: 544

TYPE: PRT

ORGANISM: Homo sapiens

US-09-910-600-8

Query Match

83.03; Score 2803.5; DB 10; Length 544;

Best Local Similarity 85.14; Pred. No. 1.9e-182;

Matches 544; Conservative 0; Mismatches 0; Indels 95; Gaps 1;

QY 1 MLPLLLSSLLGSGQAMGDFWIRVQESVMPGLGICISVPCSFSPQDWTGSTPAYGW 60

DB 1 MLPLLLSSLLGSGQAMGDFWIRVQESVMPGLGICISVPCSFSPQDWTGSTPAYGW 60

QY 61 FKAVTTTGAPVATNHQREVENMSTRGRFQLTGDPKAGKNCSLVIRDAQMDESQFFRV 120

DB 61 FKAVTTTGAPVATNHQREVENMSTRGRFQLTGDPKAGKNCSLVIRDAQMDESQFFRV 120

QY 121 ERGSYRYNFMNDGFFLKVTLSTPRPDHNTDLTCHVDSEKGVSAORTVLRVAVAP 180

DB 121 ERGSYRYNFMNDGFFLKVTLSTPRPDHNTDLTCHVDSEKGVSAORTVLRVAVAP 180

QY 181 RDIVISIRNDTPALPQPGQNNVYLEAQKGQFLRLCAADSOPPATLSWVLQNRVLSS 240

DB 181 RDIVISIRNDTPALPQPGQNNVYLEAQKGQFLRLCAADSOPPATLSWVLQNRVLSS 240

QY 241 HPWGPRLGLGLPGVKAGDSGRVTCBAENRSGQBALDLSVQYPPENLRVMVSOANRTV 300

DB 241 HPWGPRLGLGLPGVKAGDSGRVTCBAENRSGQBALDLSVQYPPENLRVMVSOANRTV 300

QY 301 LENLGNSTSLPVLEGOSLCLVCVTHSSPPARLSWTOGQVLSFSPQSDPGVLELPRVQVE 360

DB 301 LENLGNSTSLPVLEGOSLCLVCVTHSSPPARLSWTOGQVLSFSPQSDPGVLELPRVQVE 360

QY 361 HEGEFTCHARHPLGSHVLSLSVHSPKLLGPFSCSWEAEGLHCSCSSQASAPSLRWML 420

DB 361 HEGEFTCHARHPLGSHVLSLSVHSPKLLGPFSCSWEAEGLHCSCSSQASAPSLRWML 420

QY 421 GEELLEGNSQDSFEVTPSSAGSWANSLSLHGLSSGLRLCEAWNVHGAQSGSILQLP 480

DB 387 ----- 386

QY 481 DKGLISTAFSNGAFIGITALLFLCLALIMKILPKRTQTETPRPRFSHSTILYI 540

DB 387 -KKGLLSTAFSNGAFIGITALLFLCLALIMKILPKRTQTETPRPRFSHSTILYI 445

QY 541 NVVPTAGPLAOKENOKATNSPRTPLPGCAPSPESKCKOKYOQLPSPEPKSSTCAPES 600

DB 446 NVVPTAGPLAOKENOKATNSPRTPLPGCAPSPESKCKOKYOQLPSPEPKSSTCAPES 505

QY 601 QSQEELHVTALNFPQVRRPRPEARMPKGTQADYAEVKFQ 639

DB 506 QSQEELHVTALNFPQVRRPRPEARMPKGTQADYAEVKFQ 544

RESULT 10

US-09-978-295A-259

Sequence 259, Application US/09978295A

Patent No. US20020156006A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194

; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 9; Length 544;

Best Local Similarity 84.8%; Pred. No. 1.5e-181;

Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

Qy	1	MLP	LLSSLLGGSQAM	DGRFWIRVQESVMVPEGLCLISVPCSFSPQDWTG	STPAYGYW	60	
Db	1	MLP	LLSSLLGGSQAM	DGRFWIRVQESVMVPEGLCLISVPCSFSPQDWTG	STPAYGYW	60	
Qy	61	FKAV	TETTKGAPVATNHQ	REVENMSTRGRFQLTGDPKAGNC	SLVIRDAQMDQESQYFVR	120	
Db	61	FKAV	TETTKGAPVATNHQ	REVENMSTRGRFQLTGDPKAGNC	SLVIRDAQMDQESQYFVR	120	
Qy	121	ERGSYVR	YNFMNDGFFLKVT	VLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP		180	
Db	121	ERGSYVR	YNFMNDGFFLKVT	VLSTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP		180	
Qy	181	RDIVIS	SRDNTPALEPQ	QGNVPYLEAKGQFLRLICAADSQP	ATLSWVLQNRVLS	240	
Db	181	RDIVIS	SRDNTPALEPQ	QGNVPYLEAKGQFLRLICAADSQP	ATLSWVLQNRVLS	240	
Qy	241	HPWGP	PRPLGLELPGVKAGD	SGRYTCRAENRLGSOQRALDLSVQYPPENLRVMV	QANRTV	300	
Db	241	HPWGP	PRPLGLELPGVKAGD	SGRYTCRAENRLGSOQRALDLSVQYPPENLRVMV	QANRTV	300	
Qy	301	LENL	NGTSLPVL	EGQSLCLVCVTHSSPPARLSWTQ	RGVLSRQSPDPGVLELPRVQVE	360	
Db	301	LENL	NGTSLPVL	EGQSLCLVCVTHSSPPARLSWTQ	RGVLSRQSPDPGVLELPRVQVE	360	
Qy	361	HEGEFT	CHARHPLGSOHV	SLSVHVSFKLLGPSCSWEAEG	LHCSCSSQASPA	PSLRLWWL	420
Db	361	HEGEFT	CHARHPLGSOHV	SLSVHVSFKLLGPSCSWEAEG	LHCSCSSQASPA	PSLRLWWL	420
Qy	421	GEEL	EGNSSQDSPEV	TFSSAGPWANSSLSLHG	GLSLRURCEANV	HGAQSGSILQLP	480
Db	387						386

		Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;	
Qy	1	MLPLLLSLLGGSQAMDGFRWIRVOESVMVPEGLCISVPCSFSPRQDWTGTPAYGW	60
Db	1	MLPLLLSLLGGSQAMDGFRWIRVOESVMVPEGLCISVPCSFSPRQDWTGTPAYGW	60
Qy	61	FKAVTTKGAPVATNHQREVENSTRGRPOLTGDPKAGNCSLVIRDAQMDQSQFFRV	120
Db	61	FKAVTTKGAPVATNHQREVENSTRGRPOLTGDPKAGNCSLVIRDAQMDQSQFFRV	120
Qy	121	ERGSYRYNEMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSQARTVRLVAYAP	180
Db	121	ERGSYRYNEMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSQARTVRLVAYAP	180
Qy	181	RDLVISISRDNTPALEPQPGNVPYLEAQKQFRLLLCAADSOPATLSKVLQNRVLSS	240
Db	181	RDLVISISRDNTPALEPQPGNVPYLEAQKQFRLLLCAADSOPATLSKVLQNRVLSS	240
Qy	241	HPWGPRPLGLELPQVAGDSGRYTCRAENPLGSOQALDLSVOYPENLRVMYSQANRTV	300
Db	241	HPWGPRPLGLELPQVAGDSGRYTCRAENPLGSOQALDLSVOYPENLRVMYSQANRTV	300
Qy	301	LENLNGTSLPVLGGOSLCLVCTHSSPPARLSTWORGQVLSPSQSPDPCVLELPRVQVE	360
Db	301	LENLNGTSLPVLGGOSLCLVCTHSSPPARLSTWORGQVLSPSQSPDPCVLELPRVQVE	360
Qy	361	HEGEFTCHARHPLGSHVLSLSVHSPKLLGSPCSWEAEGHLHSCSSQASPAWSLWML	420
Db	361	HEGEFTCHARHPLGSHVLSLSVHSPKLLGSPCSWEAEGHLHSCSSQASPAWSLWML	420
Qy	421	GEBELGNSQDSFEVTPSSAGPWANSLSLHGGSLRCEAMNVHGAQSGSILQLP	480
Db	421	GEBELGNSQDSFEVTPSSAGPWANSLSLHGGSLRCEAMNVHGAQSGSILQLP	480
Qy	481	DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPRFSRHTILDYI	540
Db	481	DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPRFSRHTILDYI	540
Qy	541	NVPTAGPLAQKQKATNSPRTPPGAPSPESKQKQKQYQLSPFPKSTQAPES	600
Db	541	NVPTAGPLAQKQKATNSPRTPPGAPSPESKQKQKQYQLSPFPKSTQAPES	600
Qy	601	QESQELHYATLNPFGVRPRPEARMKGTQADYAEVKFQ	639
Db	601	QESQELHYATLNPFGVRPRPEARMKGTQADYAEVKFQ	639
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; Sequence 259, Application US/09978-192A			
; Patent No. US20020177553A1			
; GENERAL INFORMATION:			
; APPLICANT: Ashkenazi, Avi			
; APPLICANT: Baker Kevin P.			
; APPLICANT: Botstein, David			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Eaton, Dan			
; APPLICANT: Ferrara, Napoleon			
; APPLICANT: Filvaroff, Ellen			
; APPLICANT: Forst, Sherman			
; APPLICANT: Gao, Wei-Qiang			
; APPLICANT: Gerber, Hanspeter			
; APPLICANT: Geritsen, Mary E.			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Hillan, Kenneth J.			
; APPLICANT: Kijavina, Ivar J.			
; APPLICANT: Kuo, Sophia S.			
; APPLICANT: Napier, Mary A.			
; APPLICANT: Pan, James			
; APPLICANT: Paoni, Nicholas F.			

Query Match 82.8%; Score 2790.5; DB 9; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;

APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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1 PRIOR FILING DATE: 1998-05-15
1 PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 9; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

QY 1 MLLPILLSLLGSGAMGRFWIRVOESVMYPEGILCVPCSFYPRODWTGSTPAYGYW 60
DB 1 MLLPILLSLLGSGAMGRFWIRVOESVMYPEGILCVPCSFYPRODWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSVREVMSTRGRFQITGDPKAGNCSLVIRDAQMDESQYFRV 120
DB 61 FKAVTETTKGAPVATNHQSVREVMSTRGRFQITGDPKAGNCSLVIRDAQMDESQYFRV 120
QY 121 ERGSVVRNFMNDGFELKTVLSFTFRPDQNDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
DB 121 ERGSVVRNFMNDGFELKTVLSFTFRPDQNDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
QY 181 RDLVTSISRDNTPALEPOQGNVPYLEAKQGOFLRLCAADSQPPATLSWYLNQVLS 240
DB 181 RDLVTSISRDNTPALEPOQGNVPYLEAKQGOFLRLCAADSQPPATLSWYLNQVLS 240
QY 241 HPWGRPRIGLELPGVKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVQANRTV 300
DB 241 HPWGRPRIGLELPGVKAGDSGRYTCAENRLGSOQRALDLSVOYPPENLRVMVQANRTV 300
QY 301 LENLNGTSLPVLGQSLCLVCTVTHSSPPARLSWTQGVLSQSPSPDPGVLELPRVQVE 360
DB 301 LENLNGTSLPVLGQSLCLVCTVTHSSPPARLSWTQGVLSQSPSPDPGVLELPRVQVE 360
QY 361 HEGEFTCHARPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWL 420
DB 361 HEGEFTCHARPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWL 420
QY 386 HEGEFTCHARPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWL 386
DB 386 HEGEFTCHARPLGSHVLSVHYSPKLLGPGSCWEAGLHCSCSSQASPAFLRWL 386
QY 421 GBELEGNSSQDSFEVTTSSAGPWNANSSLSLHGLSSGLRURCEAWNVHGAQSGSILQLP 480
DB 387 ----- 386
QY 481 DKKGLISTAFNSGAFILGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYI 540
DB 387 -KKGLISTAFNSGAFILGIGITALLFLCLALIMKILPKRTQTETPRFRSHSTILDYI 445
QY 541 NVVPTAGPLAQKNQKATPNSRTPPLPGAPSPESKKNQKQYQLPSPEPKSSTQAPES 600
DB -----

DB 446 NVVPTAGPLAQKNQKATPNSRTPPLPGAPSPESKKNQKQYQLPSPEPKSSTQAPES 505
QY 601 QESQELHYATLNFPGVRRPRPEARMKPGTQADYAEVKFQ 639
DB 506 QESQELHYATLNFPGVRRPRPEARMKPGTQADYAEVKFQ 544

RESULT 13
US-09-999-832A-259
Sequence 259, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27

PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-06
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
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PRIOR APPLICATION NUMBER: 60/085339
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PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 82.6%; Score 2790.5; DB 9; Length 544;

Best Local Similarity 84.8%; Pred. No. 1.5e-181;

Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

Qy 1 MLLPILLSLLGGSQAMDGRFWIRVOESVWVPEGLICISVPCFSYPRQDWTGSTPAYGYW 60

Db 1 MLLPILLSLLGGSQAMDGRFWIRVOESVWVPEGLICISVPCFSYPRQDWTGSTPAYGYW 60

Qy 61 FXAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKGNCSLVIRDAQMQDESQVFFRV 120

Db 61 FRAVTEETKGAFAVTHQSRREVEMSTRGFOLTGDPKAGNCSLVIRDAQMDQESQYFVR 120
QY 121 ERGSVVRNFMNDGFELKVTLSFTPRQDNDTDLTCHVDPSRKGVSQRTVRLRVAYAP 180
Db 121 ERGSVVRNFMNDGFELKVTLSFTPRQDNDTDLTCHVDPSRKGVSQRTVRLRVAYAP 180
QY 181 RDLVISIRDNTPALEPQGNVPYLEAKQGFLLCAADSPATLSWLVQNRVLSS 240
Db 181 RDLVISIRDNTPALEPQGNVPYLEAKQGFLLCAADSPATLSWLVQNRVLSS 240
QY 241 HPGPRPLGLEPGVKAGSGRYTCRAENRLGSOQRALDLSVOYPPENLRVWVQANRTV 300
Db 241 HPGPRPLGLEPGVKAGSGRYTCRAENRLGSOQRALDLSVOYPPENLRVWVQANRTV 300
QY 301 LENLNGTSLPVEQSLCLVCTVTHSSPPARLSWTQRQVLSPSPDPGVLELPRVQVE 360
Db 301 LENLNGTSLPVEQSLCLVCTVTHSSPPARLSWTQRQVLSPSPDPGVLELPRVQVE 360
QY 361 HEGFTCHARPLGSHQVLSLSVHYSKLLGPSCSWAEGHLHCSCSSQASPAFSLRWL 420
Db 361 HEGFTCHARPLGSHQVLSLSVHYSKLLGPSCSWAEGHLHCSCSSQASPAFSLRWL 420
QY 421 GSELLEGSSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCEANVHGAQSGSILQLP 480
Db 387 ----- 386
QY 481 DKKGLISTAFNSGAFLGITITALLFLCLALIMKILPKRRTQETPRFRGRHSTILDYI 540
Db 387 -KKGLISTAFNSGAFLGITITALLFLCLALIMKILPKRRTQETPRFRGRHSTILDYI 445
QY 541 NVVPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQYLPSPPEKSSQAPES 600
Db 446 NVVPTAGPLAQRNOKATPNSPRTPLPGAPSPESKKNQKQYQYLPSPPEKSSQAPES 505
QY 601 QBSQBELHYATLNFVGVRPRPEARMKGTQADYAEVKFQ 639
Db 506 QBSQBELHYATLNFVGVRPRPEARMKGTQADYAEVKFQ 544

RESULT 14

US-09-978-189-259

Sequence 259, Application US/09978189

Publication No. US20030004102A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Pao, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263QPIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-05-07
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PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07

Query Match 82.6%; Score 2790.5; DB 10; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
QY 1 MLLPLLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDWTGTTPAYGYW 60
DB 1 MLLPLLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDWTGTTPAYGYW 60
QY 61 PKAVTETTKGAPVATNEHOSREVENSTRGRFQLTGDDPAKNCSLVIRDAQWQDSQYFFRV 120
DB 61 PKAVTETTKGAPVATNEHOSREVENSTRGRFQLTGDDPAKNCSLVIRDAQWQDSQYFFRV 120
QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPQDHTDLTCHVDFSRKGSVAQRTVRLVAYAP 180
DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPQDHTDLTCHVDFSRKGSVAQRTVRLVAYAP 180
QY 181 RDLVISIRONTTFALEPQPGNVFYLEAQKQFRLLLCAADSPATLSWVLQNRVLSS 240
DB 181 RDLVISIRONTTFALEPQPGNVFYLEAQKQFRLLLCAADSPATLSWVLQNRVLSS 240
QY 241 HPWGPRLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVYSQANRTV 300
DB 241 HPWGPRLGLELPGVKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVYSQANRTV 300
QY 301 LENLNGTSLPVLGGQSLCIVCTVTHSSPPARLSWTORGQVLSQSDPGLVLEPRVQVE 360
DB 301 LENLNGTSLPVLGGQSLCIVCTVTHSSPPARLSWTORGQVLSQSDPGLVLEPRVQVE 360
QY 361 HEGEFTCHARHPLGSOHVLSLSVHYSPKLLGLGSCSWEABGLHCSCSSQASPAESLRWWL 420
DB 361 HEGEFTCHARHPLGSOHVLSLSVHYSPKLLGLGSCSWEABGLHCSCSSQASPAESLRWWL 420
QY 421 GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEANWVHGAQSGSILQLP 480
DB 387 ----- 386
QY 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPRFSRSTILDYI 540
DB 387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPRFSRSTILDYI 445
QY 541 NVVPTAGLAQKXNQKATPNSRTPPPGAPSPESKKNQKQYQLPSPFPKPSSTQAPES 600
DB 446 NVVPTAGLAQKXNQKATPNSRTPPPGAPSPESKKNQKQYQLPSPFPKPSSTQAPES 505
QY 601 QESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639
DB 506 QESQEBELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 544

RESULT 15

US-09-978-608A-259
; Sequence 259, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 259
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-608A-259

Query Match 82.6%; Score 2790.5; DB 10; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.5e-181;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
Qy 1 MLPLLLSLLGSGQAWDGRFWRVQESVNVPEGLCISVPCSFSPRODWTGSTEAYGYW 60
Db 1 MLPLLLSLLGSGQAWDGRFWRVQESVNVPEGLCISVPCSFSPRODWTGSTEAYGYW 60
Qy 61 FRAVTEITTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
Db 61 FRAVTEITTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
Qy 121 ERGSYRVYFMNDGPFLLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYAP 180
Db 121 ERGSYRVYFMNDGPFLLKVTVLSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYAP 180
Qy 181 RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCAADOPPAILSWLQNRVLSSS 240
Db 181 RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCAADOPPAILSWLQNRVLSSS 240
Qy 241 HPWGPPLGLELPGVKAGSGRYTCRAENRLGSQLDLSVQYPPENLRVMVQANRTV 300
Db 241 HPWGPPLGLELPGVKAGSGRYTCRAENRLGSQLDLSVQYPPENLRVMVQANRTV 300
Qy 301 LENLNGTSLPVLEGOSLGLVCVTHSSPPARLSWTORGVLSPSQSPDGVLELPRVQVE 360
Db 301 LENLNGTSLPVLEGOSLGLVCVTHSSPPARLSWTORGVLSPSQSPDGVLELPRVQVE 360

Qy 361 HEGFTCHARHPLGSOHVLSLSLVHYSKLLGPSCSWEAEGLHCSCSSQASPAPSLRWL 420
Db 361 HEGFTCHARHPLGSOHVLSLSLVHYSKLLGPSCSWEAEGLHCSCSSQASPAPSLRWL 420
Qy 421 GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEAMVNVHGAQSGSILQLP 480
Db 421 GEELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEAMVNVHGAQSGSILQLP 480
Qy 481 DKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPFRSHSTILDYI 540
Db 481 DKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTOTETPRPFRSHSTILDYI 540
Qy 541 NVVPTAGLAQKNQKATPNSPRTPLPPGAPSPESKKNQKQYQLPSPFPKSKSTQAPES 600
Db 541 NVVPTAGLAQKNQKATPNSPRTPLPPGAPSPESKKNQKQYQLPSPFPKSKSTQAPES 600
Qy 601 QESQELHYATLNPFGVRRPEARMMPKGTQADYAEVKFQ 639
Db 601 QESQELHYATLNPFGVRRPEARMMPKGTQADYAEVKFQ 639

Search completed: November 5, 2004, 14:13:49
Job time : 112.924 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 140.458 Seconds
(without alignments)
2617.614 Million cell updates/sec

Title: US-09-937-636-4
Perfect score: 3377
Sequence: 1 MLLPILLSLLGGSQAMDGR.....RPERMPKGTQADYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: uniprot_02.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3334	98.7	697	1	SILA_HUMAN
2	2790.5	82.6	544	2	Q6UX18
3	2790.5	82.6	544	2	AAQ88703
4	2173	64.3	686	1	SILB_HUMAN
5	2108.5	62.4	425	2	BAC85493
6	1800	53.3	688	2	Q80ZE3
7	1668	49.4	623	2	Q8BY18
8	1047	31.0	551	1	SIL5_HUMAN
9	1039	30.8	551	2	AAH29896
10	837	24.8	569	1	SILF_MOUSE
11	772.5	22.9	523	2	Q80ZE2
12	721.5	21.4	499	1	SIL8_HUMAN
13	718.5	21.3	499	2	Q72728
14	700.5	20.7	595	1	SILL_HUMAN
15	692.5	20.5	597	1	SILL_PANTR
16	659.5	19.5	468	2	Q6PJ50
17	659.5	19.5	468	2	AAQ79834
18	659.5	19.5	468	2	AAQ72479
19	659.5	19.5	468	2	AAH23280
20	657.5	19.5	467	1	SIL5_MOUSE
21	640.5	19.0	463	1	SIL9_HUMAN
22	631.5	18.7	439	2	Q6GTU4
23	631	18.7	467	1	SIL7_HUMAN
24	620	18.4	394	2	Q6UXG0
25	620	18.4	394	2	AAQ88735
26	620	18.4	423	2	Q8BU57
27	607.5	18.0	442	1	SIL6_HUMAN
28	554.5	16.4	437	2	AAH35359
29	486	14.4	626	1	MAG_HUMAN
30	479	14.2	626	1	MAG_RAT
31	473	14.0	626	1	MAG_MOUSE

ALIGNMENTS

RESULT 1

ID	SILA_HUMAN	STANDARD	PRT	637 AA.
AC	Q96LC7; Q96G54; Q96LC8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Sialic acid binding Ig-like lectin 10 precursor (Siglec-10) (Siglec-like protein 2)			
GN	Name=SIGLEC10; Synonyms=SLG2;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RP	MEDLINE=21303047; PubMed=11409878; DOI=10.1006/bbrc.2001.5053;			
RA	Yousef G.M., Ordon M.H., Fousias G., Diamandis E.P.;			
RT	"Molecular characterization, tissue expression, and mapping of a novel Siglec-like gene (SLG2) with three splice variants.";			
RL	Biochem. Biophys. Res. Commun. 284:900-910(2001).			
[2]	SEQUENCE FROM N.A. (ISOFORM 1).			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Spleen;			
RA	MEDLINE=21181594; PubMed=11284738;			
RA	Munday J., Kerr S., Ni J., Cornish A.L., Zhang J.Q., Nicoll G.,			
RA	Floyd H., Mattei M.-G., Moore P., Liu D., Crocker P.R.;			
RT	"Identification, characterization and leucocyte expression of Siglec-10, a novel human sialic acid-binding receptor.";			
RL	Biochem. J. 355:489-497(2001).			
[3]	SEQUENCE FROM N.A. (ISOFORM 2).			
RP	TISSUE=Dendritic cell;			
RA	MEDLINE=21359381; PubMed=11358961; DOI=10.1074/jbc.M100467200;			
RA	Li N., Zhang W., Wan T., Zhang J., Chen T., Yu Y., Wang J., Cao X.;			
RT	"Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells.";			
RL	J. Biol. Chem. 276:28106-28112(2001).			
[4]	SEQUENCE FROM N.A. (ISOFORM 3), ALTERNATIVE SPLICING (ISOFORMS 4 AND 5), MUTAGENESIS OF TYR-667, AND INTERACTION WITH PTPN6.			
RP	MEDLINE=22152890; PubMed=12163025; DOI=10.1016/S0006-291X(02)00885-9;			
RA	Kitzig F., Martinez-Barriocanal A., Lopez-Botet M., Sayos J.;			
RT	"Cloning of two new splice variants of Siglec-10 and mapping of the interaction between Siglec-10 and SHP-1.";			
RL	Biochem. Biophys. Res. Commun. 296:355-362(2002).			
[5]	SEQUENCE OF 337-697 FROM N.A. (ISOFORM 1/3/4).			
RP	SEQUENCE=B-cell;			
RC	TISSUE=B-cell;			
RA	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straussberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haeh F.,			

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 Proc Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3- or 2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatases) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules.
 CC -1- SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1-4); secreted (isoform 5).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q96LC7-1; Sequences=Displayed;
 CC Name=2; Synonyms=Short, Sv1;
 CC IsoId=Q96LC7-2; Sequences=VSP_002565;
 CC Name=3; Synonyms=Sv3;
 CC IsoId=Q96LC7-3; Sequences=VSP_002564;
 CC Name=4; Synonyms=Sv4;
 CC IsoId=Q96LC7-4; Sequences=VSP_002561;
 CC Name=5; Synonyms=Sv2;
 CC IsoId=Q96LC7-5; Sequences=VSP_002563;
 CC TISSUE SPECIFICITY: Expressed by peripheral blood leukocytes (eosinophils, monocytes and a natural killer cell subpopulation). Isoform 5 is found to be the most abundant isoform. Found in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal chord. Isoform 2 is also found in brain. Isoform 4 is specifically found in natural killer cells.
 CC -1- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
 CC -1- PTM: Phosphorylation of Tyr-667 is involved in binding to PTPN6.
 CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily, SIGLEC (sialic acid binding Ig-like lectin) family.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AY029277; AAK40255.1; -
 CC EMBL: AY029277; AAK40256.1; -
 CC EMBL: AF310233; AAK55139.1; -
 CC EMBL: AF311905; AAK92542.1; -
 CC EMBL: AY032685; AAK51124.1; -
 CC EMBL: BC003955; AAK03955.2; -
 CC HSP: Q9Y286; 1075.

DR Genew: HGNC:15620; SIGLEC10.
 DR MIN; 606091;
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SMO0408; IGc2; 2.
 DR PROSITE: PS00835; IG LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Alternative splicing; Cell adhesion; Glycoprotein;
 KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 16 Potential.
 FT CHAIN 17 697 Sialic acid binding Ig-like lectin 10.
 FT DOMAIN 17 550 Extracellular (Potential).
 FT TRANSEM 551 571 Potential.
 FT DOMAIN 572 697 Cytoplasmic (Potential).
 FT DOMAIN 18 121 Ig-like V-type.
 FT DOMAIN 146 231 Ig-like C2-type 1.
 FT DOMAIN 251 339 Ig-like C2-type 2.
 FT DOMAIN 344 441 Ig-like C2-type 3.
 FT SITE 595 600 ITIM motif 1.
 FT SITE 665 670 ITIM motif 2.
 FT DISULFID 36 173 By similarity.
 FT DISULFID 41 101 By similarity.
 FT DISULFID 164 215 By similarity.
 FT DISULFID 276 323 By similarity.
 FT DISULFID 380 425 By similarity.
 FT MOD RES 667 667 Phosphotyrosine.
 FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 486 486 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 504 504 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 125 214 Missing (in isoform 4).
 FT FTID=VSP_002561.
 FT TALTQPDVTPITLPGQPVTVCVFNWAFECPPPSFSW
 FT TGAAL -> TGMWGNPCLSHMGGTGTATGLSRGSGQP
 FT LQHNLPERSLSQP (in isoform 5).
 FT FTID=VSP_002562.
 FT Missing (in isoform 5).
 FT FTID=VSP_002563.
 FT Missing (in isoform 3).
 FT FTID=VSP_002564.
 FT Missing (in isoform 2).
 FT FTID=VSP_002565.
 FT Y->F: Abolishes binding to PTPN6.
 FT CONFLICT 28 28 S -> P (in Ref. 4).
 FT CONFLICT 134 134 G -> R (in Ref. 4).
 FT CONFLICT 226 226 V -> A (in Ref. 1).
 FT CONFLICT 344 344 P -> S (in Ref. 3).
 FT CONFLICT 440 440 L -> P (in Ref. 4).
 FT CONFLICT 587 587 R -> K (in Ref. 3).
 FT CONFLICT 625 625 P -> S (in Ref. 3).
 SQ SEQUENCE 697 AA; 76619 MW; 6CB231CB49411D1B CRC64;
 Query Match 98.7%; Score 3334; DB 1; Length 697;
 Best Local Similarity 91.5%; Pred. No. 2.8e-202;
 Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;
 Qy 1 MLLPLLSLSLGGSQAMDGFRVIRVQESVYVPEGLCISVPCSFSPYPRQDMGTSTPAYGW 60
 Db 1 MLLPLLSLSLGGSQAMDGFRVIRVQESVYVPEGLCISVPCSFSPYPRQDMGTSTPAYGW 60
 Qy 61 FKAVTTTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSLVIRDAQKQDESQYFFSV 120
 Db 61 FKAVTTTKGAPVATNHQSRREVEMSTRGRFQLTGDPKAGNCSLVIRDAQKQDESQYFFSV 120
 Qy 121 ERGSYVYVNFMDGFFLKVT ----- 140
 Db 121 ERGSYVYVNFMDGFFLKVT ----- 140
 Qy 121 ERGSYVYVNFMDGFFLKVT ----- 140
 Db 121 ERGSYVYVNFMDGFFLKVT ----- 140
 Qy 141 -----VLSTPTPQDHTDITLCTHVDFSRKGVSQRTVRLRVAYAPRD 182

Db 181 TGAALSSGKTPTSHFVSFTFRPQDNDTDLCHVDVFSKGVSVQRTVLRVAYAPRD 240
Qy 183 LVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWLNQNVLSSSH 242
Db 241 LVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWLNQNVLSSSH 300
Qy 243 WGPRLGLGLPGVKAAGDSGRYTCRAENLGSQQRALDLSVQYPPENLRVMVSOANRTVLE 302
Db 301 WGPRLGLGLPGVKAAGDSGRYTCRAENLGSQQRALDLSVQYPPENLRVMVSOANRTVLE 360
Qy 303 NLNGNTSLFVLGQSLCLVCTHSPFARLSTQRGQVLSQSPSDPGVLELPRVQVEHE 362
Db 361 NLNGNTSLFVLGQSLCLVCTHSPFARLSTQRGQVLSQSPSDPGVLELPRVQVEHE 420
Qy 363 GEFTCHARHPLGSHVLSLSVHYSPKLLGSPCSWEAEGHLCSSQSPAPSLRWLGE 422
Db 421 GEFTCHARHPLGSHVLSLSVHYSPKLLGSPCSWEAEGHLCSSQSPAPSLRWLGE 480
Qy 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGSLSSGLRLRCEAMNVHGAQSGSILQLPDK 482
Db 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGSLSSGLRLRCEAMNVHGAQSGSILQLPDK 540
Qy 483 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYINV 542
Db 541 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYINV 600
Qy 543 VPTAGPLAQRNOKATNSPRTPPLPGAPSPESKKNQKQYOLPSPFPKSTQAPESQ 602
Db 601 VPTAGPLAQRNOKATNSPRTPPLPGAPSPESKKNQKQYOLPSPFPKSTQAPESQ 660
Qy 603 SQEELHYATLNFPGVVRPPEARMKPGTQADYAEVKFQ 639
Db 661 SQEELHYATLNFPGVVRPPEARMKPGTQADYAEVKFQ 697

DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 544 AA; 60267 MW; 4D4E1BFD60AC8CB CRC64;
Query Match 82.8%; Score 2790.5; DB 2; Length 544;
Best Local Similarity 84.8%; Pred. No. 4.4e-168;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
Qy 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Db 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy 61 FKAVTTETTKGAPVATNHQSEVENSTGRFQLTGDPAKGNCSLVIRDAQMDQDSQFFRV 120
Db 61 FKAVTTETTKGAPVATNHQSEVENSTGRFQLTGDPAKGNCSLVIRDAQMDQDSQFFRV 120
Qy 121 ERGSYVRYNEMNDGFTLVTLSTFRPDQDHTDLCHVDVFSKGVSAQRTVLRVAYAP 180
Db 121 ERGSYVRYNEMNDGFTLVTLSTFRPDQDHTDLCHVDVFSKGVSAQRTVLRVAYAP 180
Qy 181 RDVLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWLNQNVLSSSH 240
Db 181 RDVLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWLNQNVLSSSH 240
Qy 241 HPKGPRLGLGLPGVKAAGDSGRYTCRAENLGSQQRALDLSVQYPPENLRVMVSOANRTV 300
Db 241 HPKGPRLGLGLPGVKAAGDSGRYTCRAENLGSQQRALDLSVQYPPENLRVMVSOANRTV 300
Qy 301 LENLNGTSLFVLGQSLCLVCTHSPFARLSTQRGQVLSQSPSDPGVLELPRVQVE 360
Db 301 LENLNGTSLFVLGQSLCLVCTHSPFARLSTQRGQVLSQSPSDPGVLELPRVQVE 360
Qy 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGSPCSWEAEGHLCSSQSPAPSLRWL 420
Db 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGSPCSWEAEGHLCSSQSPAPSLRWL 480
Qy 421 GEELEGNSSQDSFEVTPSSAGPWANSSLSLHGSLSSGLRLRCEAMNVHGAQSGSILQLP 480
Db 387 ----- 386
Qy 481 DKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYI 540
Db 387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYI 445
Qy 541 NVPTAGPLAQRNOKATNSPRTPPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 600
Db 446 NVPTAGPLAQRNOKATNSPRTPPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 505
Qy 601 QESQEBELHYATLNFPGVVRPPEARMKPGTQADYAEVKFQ 639
Db 506 QESQEBELHYATLNFPGVVRPPEARMKPGTQADYAEVKFQ 544

RESULT 3
AAQ88703
ID AAQ88703 PRELIMINARY; PRT; 544 AA.
AC AAQ88703
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE SIGLEC10.
GN ORFNames=UNQ477;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358337; AAQ88703.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 2.

DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 544 AA; 60267 MW; 4D4E1BFD60AC8CB CRC64;
Query Match 82.8%; Score 2790.5; DB 2; Length 544;
Best Local Similarity 84.8%; Pred. No. 4.4e-168;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;
Qy 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Db 1 MLLPLLLSSLLGSGQAMDGRFWIRVOESVNVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
Qy 61 FKAVTTETTKGAPVATNHQSEVENSTGRFQLTGDPAKGNCSLVIRDAQMDQDSQFFRV 120
Db 61 FKAVTTETTKGAPVATNHQSEVENSTGRFQLTGDPAKGNCSLVIRDAQMDQDSQFFRV 120
Qy 121 ERGSYVRYNEMNDGFTLVTLSTFRPDQDHTDLCHVDVFSKGVSAQRTVLRVAYAP 180
Db 121 ERGSYVRYNEMNDGFTLVTLSTFRPDQDHTDLCHVDVFSKGVSAQRTVLRVAYAP 180
Qy 181 RDVLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWLNQNVLSSSH 240
Db 181 RDVLVISISRDNTPALEPQGNVPYLEAQKQFLRLCAADSPATLSWLNQNVLSSSH 240
Qy 241 HPKGPRLGLGLPGVKAAGDSGRYTCRAENLGSQQRALDLSVQYPPENLRVMVSOANRTV 300
Db 241 HPKGPRLGLGLPGVKAAGDSGRYTCRAENLGSQQRALDLSVQYPPENLRVMVSOANRTV 300
Qy 301 LENLNGTSLFVLGQSLCLVCTHSPFARLSTQRGQVLSQSPSDPGVLELPRVQVE 360
Db 301 LENLNGTSLFVLGQSLCLVCTHSPFARLSTQRGQVLSQSPSDPGVLELPRVQVE 360
Qy 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGSPCSWEAEGHLCSSQSPAPSLRWL 420
Db 361 HEGEFTCHARHPLGSHVLSLSVHYSPKLLGSPCSWEAEGHLCSSQSPAPSLRWL 480
Qy 421 GEELEGNSSQDSFEVTPSSAGPWANSSLSLHGSLSSGLRLRCEAMNVHGAQSGSILQLP 480
Db 387 ----- 386
Qy 481 DKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYI 540
Db 387 -KKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTQTETPRPFRSHSTILDYI 445
Qy 541 NVPTAGPLAQRNOKATNSPRTPPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 600
Db 446 NVPTAGPLAQRNOKATNSPRTPPLPGAPSPESKKNQKQYOLPSPFPKSTQAPES 505
Qy 601 QESQEBELHYATLNFPGVVRPPEARMKPGTQADYAEVKFQ 639
Db 506 QESQEBELHYATLNFPGVVRPPEARMKPGTQADYAEVKFQ 544

Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P.;
 "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
 Bioinformatics Assessment.";
 Genome Res. 13:2265-2270(2003).
 EMBL; AY358337; AAQ88703.1; -.
 J. Biol. Chem. 277:24466-24474(2002).
 SEQUENCE 544 AA; 60267 MW; 4DA4E1EDF60AC8CB CRC64;

Query Match 82.6%; Score 2790.5; DB 2; Length 544;
 Best Local Similarity 84.8%; Pred. No. 4.4e-168;
 Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

QY 1 MLLPLLLSSLLGGSQANDGRFWIRVOESVNMVPEGLCISVPCFSYPRQDWTGTPAYGYW 60
 DB 1 MLLPLLLSSLLGGSQANDGRFWIRVOESVNMVPEGLCISVPCFSYPRQDWTGTPAYGYW 60
 QY 61 FKAVTTTKAPVATNHQSEVEMSTRGRFQLTGDPKAGKNCISIVTDAQMDQESQFFRV 120
 DB 61 FKAVTTTKAPVATNHQSEVEMSTRGRFQLTGDPKAGKNCISIVTDAQMDQESQFFRV 120
 QY 121 ERGSYVYPMNDGFFELKVTLSFTPRQDHTDLCHVDLFRKGVSAQRTVLRVAVAP 180
 DB 121 ERGSYVYPMNDGFFELKVTLSFTPRQDHTDLCHVDLFRKGVSAQRTVLRVAVAP 180
 QY 181 RLIVISIRNDTALBPQGNVYLEAQGFRLLCADQOPATLSWLVQNRVLSS 240
 DB 181 RLIVISIRNDTALBPQGNVYLEAQGFRLLCADQOPATLSWLVQNRVLSS 240
 QY 241 HPWGPRLGLPLGVKAGDSGRVTCRAENRLGSGQBALDLSVQYPPENLRVMVQANRTV 300
 DB 241 HPWGPRLGLPLGVKAGDSGRVTCRAENRLGSGQBALDLSVQYPPENLRVMVQANRTV 300
 QY 301 LENLNGTSLVPLEGQSLCIVCVTHSSPPARLSWTORGVLSPSPQSDPGLPRVQVE 360
 DB 301 LENLNGTSLVPLEGQSLCIVCVTHSSPPARLSWTORGVLSPSPQSDPGLPRVQVE 360
 QY 361 HEGETTCHARHPLGSHVLSLSVHYSVKLLGPSCSWEAEGLHCSCSSQASAPSLRWL 420
 DB 361 HEGETTCHARHPLGSHVLSLSVHYSVKLLGPSCSWEAEGLHCSCSSQASAPSLRWL 420
 QY 421 GBELEGNSSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLCEANVHGAGSILQLP 480
 DB 387 ----- 386
 QY 481 DKGLISTAFSGAFIGITALLFLCLALITKILPKRTOTETPRFSSHSTILDYI 540
 DB 387 -XKGLISTAFSGAFIGITALLFLCLALITKILPKRTOTETPRFSSHSTILDYI 445
 QY 541 NVVETAGPLAQKRNQKATNSPRTPLPGAPSPESKKNQKQYQLPSPPEKSSQAPES 600
 DB 446 NVVETAGPLAQKRNQKATNSPRTPLPGAPSPESKKNQKQYQLPSPPEKSSQAPES 505
 QY 601 QESQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 639
 DB 506 QESQELHYATLNFQVRPRPAPKPGTQADYAEVKFQ 544

RESULT 4

ID SILB HUMAN STANDARD; PRT; 686 AA.
 AC Q96RL6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic
 acid-binding lectin 11) (UNQ9222/PRO28718).
 GN Name=SIGLEC11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 OX MEDLINE=22887296; PubMed=11986327; DOI=10.1074/jbc.M202833200;
 RN MEDLINE=22086217; PubMed=11986327; DOI=10.1074/jbc.M202833200;
 RP Angeta T., Kerr S.C., Greaves D.R., Varki N.M., Crocker P.R.,
 Varki A.;
 RA "Cloning and characterization of human Siglec-11. A recently evolved
 RT signaling that can interact with SHP-1 and SHP-2 and is expressed by
 RT tissue macrophages, including brain microglia.";
 RL J. Biol. Chem. 277:24466-24474(2002).
 [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
 Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P., Gray A.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 CC dependent binding to cells. Preferentially binds to alpha2,8-
 CC linked sialic acid. The sialic acid recognition site may be masked
 CC by cis interactions with sialic acids on the same cell surface. In
 CC the immune response, may act as an inhibitory receptor upon ligand
 CC induced tyrosine phosphorylation by recruiting cytoplasmic
 CC phosphatase(s) via their SH2 domain(s) that block signal
 CC transduction through dephosphorylation of signaling molecules.
 CC -!- SUBUNIT: Interacts with PTPN6/SHP-1 and PTPN11/SHP-2 upon
 CC phosphorylation.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q96RL6-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q96RL6-2; Sequence=VSP_008764;
 CC -!- TISSUE SPECIFICITY: Expressed by macrophages in various tissues
 CC including Kupffer cells. Also found in brain microglia.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
 CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 CC motif is involved in modulation of cellular responses. The SH2-
 CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
 CC containing phosphatases.
 CC -!- PTM: Phosphorylated on tyrosine residues.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
 CC (sialic acid binding Ig-like lectin) family.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF37818; AAQ72907.1; -.
 CC EMBL; AY358135; AAQ88502.1; -.
 CC HSP; Q9V286; 107S.
 CC Genew; HGNC:15622; SIGLEC11.
 CC MIM; 607157; -.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 3.

DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 1.
KW Alternative splicing; Cell adhesion; Glycoprotein;
KW Immunoglobulin domain; Lectin; Phosphorylation; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 15 Potential.
FT CHAIN 16 686 Sialic acid binding Ig-like lectin 11.
FT DOMAIN 16 549 Extracellular (Potential).
FT TRANSMEM 550 572 Potential.
FT DOMAIN 573 686 Cytoplasmic (Potential).
FT DOMAIN 19 122 Ig-like V-type.
FT DOMAIN 147 232 Ig-like C2-type 1.
FT DOMAIN 229 338 Ig-like C2-type 2.
FT DOMAIN 343 440 Ig-like C2-type 3.
FT SITE 630 635 ITIM motif.
FT DISULFID 37 174 By similarity.
FT DISULFID 42 102 By similarity.
FT DISULFID 165 216 By similarity.
FT DISULFID 275 322 By similarity.
FT DISULFID 379 424 By similarity.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 250 250 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 354 354 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 363 363 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 485 485 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 503 503 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 443 539 YPQLGPSWEAGELHCSSQSPAPSLRWLGEELLE
GNSSQGSFEVTPSSAGPWANSLSLHGLSSGLRLRCRAWN
VFGAQSQVFLPLPG -> W (in isoform 2).
/FTID=VSP_008764.
FT CONFLICT 84 84 E -> A (in Ref. 2).
FT CONFLICT 353 353 A -> G (in Ref. 2).
FT SEQUENCE 686 AA; 74544 MW; FDEA193615685A8 CRC64;
Query Match 64.3%; Score 2173; DB 1; Length 686;
Best Local Similarity 63.3%; Pred. No. 6.2e-129;
Matches 440; Conservative 50; Mismatches 111; Indels 94; Gaps 6;
QY 1 MLPLILLSLGGSQMDCGRFWRVQESVMVEGLCISVPCSFSPYRQDWTGSTPAYGVW 60
DB 2 LLLPLLPVLGSLNKPDSYLVQVRQVPVEGLCVIVSCNLSYPRDGDWDESTAYGVW 61
QY 61 FRAVETTTKGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESYFFRV 120
DB 62 FGRGTSFKTGAPVATNHQREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDQESYFFRV 121
QY 121 ERGSYVRYNFMNDGPKLVKT----- 140
DB 122 ERGSYVRYNFMNDGPKLVKT----- 140
QY 141 -----VLSPTRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAVAPRD 182
DB 182 TGAALSPRTRTSTSHFSVLSFTFPQDHDHDLTCHVDFSRKGVSAQRTVRLRVAVAPKD 241
QY 183 LVTSISRDNTPALEPOQGNVYLEAKQKQFRLLLCAADSQPPATLSWYLNVRVSSSHP 242
DB 242 LAISISHDNTSALE--LQGNVILEYKQKQFRLLLCAADSQPPATLSWYLNVRVSSSHP 299
QY 243 WGRPPLGLELPVKGAGDSGRYTCRAENRLGSOORALDLSVQYPPENLRVMVSOANRTVLE 302
DB 300 WGRPTLGLRUGRVAGDSGRYTCRAENRLGSOOQALDLSVQYPPENLRVMVSOANRTVLE 359
QY 303 NLNGNGTSLPVLGQSLCVVTHSSPPARLSWTQGVLSPPQSPDPGVLELPVQVHEHE 362
DB 360 NLNGNGTSLPVLGQSLRLVCVTHSSPPARLSWTQGVLSPPQSPDPGVLELPVQVHEHE 419
QY 363 GEFTCHARPLGSHVLSLSVHYSPKLLGPSCSWEAGELHCSSQSPAPSLRWLWGE 422
DB 420 GEFTCHARPLGSHVLSLSVHYSPKLLGPSCSWEAGELHCSSQSPAPSLRWLWGE 479
QY 423 ELLEGNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCRAWNVHGASQSIILQDPK 482

DB 480 ELLEGNSQDSFEVTPSSAGPWANSLSLHGLSSGLRLRCRAWNVHGASQSVFOLLPG 539
QY 483 KGLISTAFSNGAFGLGIGITALFLCLALIMKILPKRTQTETPRFRFSRHSTILDYINV 542
DB 540 KLEHGGGLGLGAALGAGVAALLAFCSCLVFRVKICRK-----EARKFAAAEQ-----DV 589
QY 543 VPTRAGPLAOKENKATPNSPRTPLPGAPSPSKCKQKQYQLPSPPEKSSSTQAPESQE 602
DB 590 PSTLGPISQGHQHECSAGSSQDHPPPGA-----AYTPQKGE 626
QY 603 SQBELHYATLNFPGVRPRPEARMKPGTQADYAEVK 637
DB 627 EQ-ELHYASLSFQGLRLWEPAQDEAPSTTEYSIK 660
RESULT 5
BAC85493 PRELIMINARY; PRT; 425 AA.
ID BAC85493 AC BAC85493; DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CDNA FLJ16033 fis, clone SPLEN2001599, weakly similar to Homo sapiens
DE sialic acid binding immunoglobulin-like lectin 8 long splice variant
DE (Siglec8) gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsubi T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuo Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK122619; BAC85493.1; --
KW Lectin.
SQ SEQUENCE 425 AA; 47345 MW; 809854127B397D73 CRC64;
Query Match 62.4%; Score 2108.5; DB 2; Length 425;
Best Local Similarity 69.0%; Pred. No. 4e-125;
Matches 421; Conservative 1; Mismatches 3; Indels 185; Gaps 2;
QY 30 MVPEGLCISVPCSFSPYRQDWTGSTPAYGVWFKAVTTETTKGAPVATNHQREVEMSTRGR 89
DB 1 MVPEGLCISVPCSFSPYRQDWTGSTPAYGVWFKAVTTETTKGAPVATNHQREVEMSTRGR 60
QY 90 FOLTGDPKAGNCSLVIRDAQMDQESYFFRVGRSVRYNFMNDGFLKVTLSFTPRPQ 149
DB 61 FOLTGDPKAGNCSLVIRDAQMDQESYFFRVGRSVRYNFMNDGFLKVTLSFTPRPQ 120
QY 150 DHNTDLTCHVDVFSRKGVSQRTVRLRVAVAPRDLSISRDNTPALEPQPGQGNVYLEAQ 209
DB 121 DHNTDLTCHVDVFSRKGVSQRTVRLRVAVAPRDLSISRDNTPALEPQPGQGNVYLEAQ 165
QY 210 KGQFRLLLCAADSQPPATLSWYLNVRVLSSSHPPGRLGLELPGVKAGDSGRYTCRAEN 269
DB 166 ----- 165
QY 270 RLGSQORALDLSVQYPPENLRVMVSOANRTVLENLNGTSLPVLGQSLCVVTHSSPP 329
DB 166 -----PENLRVMVSOANRTVLENLNGTSLPVLGQSLCVVTHSSPP 210
QY 330 ARLSWTQGVLSPPQSPDPGVLELPVQVHEHEGEFTCHARHPLGSHVLSLSVHYSPK 389
DB 211 ARLSWTQGVLSPPQSPDPGVLELPVQVHEHEGEFTCHARHPLGSHVLSLSVHYSPK 267

QY 390 LLGSPSCWEAEGHLCSCSQASPAPSLRWMLGELLGNSQDSFVTPSSAGPWANSSL 449
 DB 268 ----- 267
 QY 450 SLHGLSSGLRLRCEANVHGAOSGLQDPKKGLISTAFSNGAFGLGITALLFLCLA 509
 DB 268 -----KKGLISTAFSNGAFGLGITALLFLCLA 295
 QY 510 LIIMKILPKRTOTETPRPFSRSHSTILDYINVVPTAGPLAOKNOKATPNSPRTPLPG 569
 DB 296 LIIMKILPKRTOTETPRPFSRSHSTILDYINVVPTAGPLAOKNOKATPNSPRTPLPG 355
 QY 570 APSPEKKNKKQYQLPSPFPPEKSSSTQAPESQBSQELHYATLNFPGVPRPEARMKGT 629
 DB 356 APSPEKKNKKQYQLPSPFPPEKSSSTQAPESQBSQELHYATLNFPGVPRPEARMKGT 415
 QY 630 QADYAEVKFQ 639
 DB 416 QADYAEVKFQ 425

RESULT 6

Q80ZE3 PRELIMINARY; PRT; 688 AA.
 AC Q80ZE3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Siglec-G.
 GN Name=Siglec10;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=22921108; PubMed=14559209;
 WA Aizawa H., Zimmermann N., Carrigan P.E., Lee J.J., Rothenberg M.E.,
 RA Bochner B.S.;
 RT "Molecular analysis of human Siglec-8 orthologs relevant to mouse
 RT eosinophils: identification of mouse orthologs of Siglec-5 (mSiglec-F)
 RT and Siglec-10 (mSiglec-G).";
 RT Genomics 82:521-530(2003).
 DR EMBL; AY216400; AAC48273.1; -.
 DR HSSP; Q9Y286; I07S.
 DR MGD; MGI:2443630; Siglec10.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG_c2.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00408; IGc2; 2.
 DR PROSITE; PS50835; IG_LIKE; 3.
 SQ SEQUENCE 688 AA; 76884 MW; 21A619B1500BFA76 CRC64;

Query Match

Best Local Similarity 54.9%; Pred. No. 2.3e-105;

Matches 381; Conservative 70; Mismatches 175; Indels 68; Gaps 9;

QY 2 LLPLLSLLSGSQMDGRFWRTRVESVMVPEGLICIVPCSPFYPRQDWTGSTAYGWYF 61
 DB 3 LLFLLSLLSFLDGPQGMESYFLQVQIRVKAQEGLCIFVPCSPFSSPEGKWLRSFLYGYWF 62
 QY 62 KAVTETTKAPVATNHSQREVMSRGRFQLTGDPKAGNCSLVIRDAQWDSQVFFRVE 121
 DB 63 KGRKPSLSFPVATNNKOKLWEARGFQLLGDSIKKNCILLIKDVWGDSYFFRME 122
 QY 122 RGSYVRYNFMN-----DGFPLKY----- 139
 DB 123 RG-FRFPFKERFLQVEALTKQDIFIPVLEPGEPVTVVCLFSWTFNQCPAPSFWSMG 181
 QY 140 -----TVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAVAPRDLV 184

DB 182 DAVSFQESRPHTSNVSVLSFIPGLQHDELTCLQDFSR--MSTQRTVRLRVAVAPRSLA 239
 QY 185 ISIREDNTPALEPOQGNVPYLEAKQGFIRLLCAADSOPATILSWLQNRVLSSHPWG 244
 DB 240 ISIFHDNVSV--PDHENPSPHLEVOQCGSLRLCTADSQPPATLSWLELDQVJWSVSPVG 297
 QY 245 PRPLGLEPGVKAGDSGRYTCRAENRLGSOQARLDLSVOYFPPENLRVMVQANRTVLENL 304
 DB 258 SRTLALSLPWKAGDSGHYTCQENRLGSOQHTLDLSVLYPQDLRTVQANRTVLEIL 357
 QY 305 GNGTSLPVLBQSLCLVCVTHSSPPARLSWTQGVLSQPSQSDPGVLELPRVQVHEGE 364
 DB 358 RNALSLPVLBQSLCLVCVTVSNPPANVSWAWVTQTLPISSEPGVLELPLVQREHEGE 417
 QY 365 FTCHARPLGSOHVSLSLVHYSPLKLGPCSWAEGLHCSCSQASQASPAPSLRWMLGEEL 424
 DB 418 FTCAQNPGLQARISLSLVHYPPQMSPPSCSWAEGLHCNCSSRAWPAFSLRWLGEGL 477
 QY 425 LEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCEANVHGAOSGLIQLPDKKG 484
 DB 478 LEGNSSNASFTVTFSSSLGPWVNSLSLLQELGPSLWLSCESWNTHGAQTTSVLLLPDKOS 537
 QY 485 LISTAFSNGAFGLGITALLFLCLALIIIMKILPKRTQTETPRPFSRSHSTILDYINVP 544
 DB 538 --ATAFSKGAVLGFGITALLALCLIVIVTKLQKGTQEPSPKLSRGSTILDYINVP 595
 QY 545 TAGPLAOKNOKATPNSPRTPLPGAPSPESKKNQK-KOYQLSPFPPEKSSSTQAPESQES 603
 DB 596 KTRSLA--RNWKAEPDAPSSRSLDTHFPKPKKQKDPHTTYPGCPDPTSSSQVPVSENN 653
 QY 604 QEELHYATLNFPGVPRPEARMKGTQADYAEVK 637
 DB 654 PEELHYAALNPSRLRQ-ETQDPQTYSDYTEVR 686

RESULT 7

Q8BY18 PRELIMINARY; PRT; 623 AA.
 ID Q8BY18;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
 DE library, clone:A630096C01 product:weakly similar to SIALIC ACID-
 DE BINDING LECTIN (Fragment).
 GN Name=Siglec10;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]

Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M., Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Dettler J.C., Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M., Glavina T., Gomez M., Gonzales E., Groza M., Hamon N., Hawkins T., Haydu L., He I., Huang W., Israni S., Jett J., Kadner K., Kimball H., Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Nelson K., Nolan M., Ovcharenko I., Pittluck S., Pollard M., Popkie A.P., Predki P., Quan G., Ramirez L., Raeh S., Retterer J., Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D., Slezak T., Solovoyev V., Thayer N., Tice H., Tsai M., Ustaszewska A., Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I., Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E., Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M., Rubin E.M., Lucas S.M.;
 RA "The DNA sequence and biology of human chromosome 19";
 RL Nature 428:529-535(2004).
 CC -I- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Binds equally to alpha2,3-linked and alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells. Found at high levels in peripheral blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing early stages of myelomonocytic differentiation.
 CC -I- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in modulation of cellular responses. The phosphorylated ITIM motif can bind the SH2 domain of several SH2-containing phosphatases.
 CC -I- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (sialic acid binding Ig-like lectin) family.
 CC -I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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 DR EMBL; AF170484; RAD50978.1; -;
 DR EMBL; U71393; AAF70703.1; -;
 DR EMBL; AC018755; AAF87846.1; -;
 DR HSSP; Q9Y286; 107S.
 DR Genew; HGNC:10874; SIGLEC5.
 DR MIM; 604200; -;
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00408; IGC2; 1.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Antigen; Cell adhesion; Glycoprotein; Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 16
 FT CHAIN 17 551
 FT DOMAIN 17 441
 FT TRANSMEM 442 462
 FT DOMAIN 463 551
 FT DOMAIN 19 136
 FT DOMAIN 146 228
 FT DOMAIN 236 330
 FT SITE 518 523
 FT SITE 542 547
 FT DISULFID 36 170
 By similarity.

FT DISULFID 41 101 By similarity.
 FT DISULFID 164 213 By similarity.
 FT DISULFID 269 314 By similarity.
 FT CARBOHYD 100 100 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 210 210 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 231 231 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 253 253 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 328 328 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 384 384 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 393 393 N-linked (GlcNAc...) (Potential).
 FT VARIANT 72 72 V -> A (in dbSNP:1973019).
 FT VARIANT 215 215 M -> V (in dbSNP:1807124).
 FT VARIANT 322 322 P -> S (in dbSNP:2278831).
 FT CONFLICT 309 309 E -> K (in Ref. 1).
 FT CONFLICT 358 358 R -> W (in Ref. 1).
 FT CONFLICT 388 388 A -> P (in Ref. 1).
 FT CONFLICT 403 403 S -> N (in Ref. 1).
 SQ SEQUENCE 551 AA; 60715 MW; 2FEA2B6B341EPEAF CRC64;
 Query Match 31.0%; Score 1047; DB 1; Length 551;
 Best Local Similarity 39.4%; Pred. No. 6.6e-58;
 Matches 256; Conservative 76; Mismatches 203; Indels 114; Gaps 15;
 QY 2 LPLLLSL- GGSQAMDGSEFWVQESVNVVPGLCISVPCSPSYPRQDTGTTPAYGW 60
 DB 1 MLPULLPLWGLGSLQKPVYELQVQKSVTVQGLCVLPVPCSPSYPRWSYSEPLVYW 60
 QY 61 FKAVTTKGAIVATNQHSSEVEMSTRGQLTGPAGKNCISVIRDAQMDQSDQVFRV 120
 DB 61 FRDGEIPYAEVAVATNPNDRVRKPEVQGRFLLGVDVQKNCISIGDARMEDTGSYFFRV 120
 QY 121 ERGSYVYFNWMDGFLKVTVLVSTFRPQDHTDLCVDFSRKGSQAQTVRLVAYAP 180
 DB 121 ERGRDVKYSQQKNLNEVTL- - - - - 142
 QY 181 RDLVISRDNTPALEPQPGNVVYLEAQKQFLRLLC- - - - - AADSQPATLSVVLQNRV 236
 DB 143 - - - - - LKEDIHLEP- - - - - LESGRFRLSCSLPGSCAAGPLTFST- - - - - GNA 184
 QY 237 LSSSHMPGPRPLGLELPGVAGSGRYTCDAENRGSQ- - - - - QALDLSVQYPPENLRMV 293
 DB 185 LSPLEDPETTRSSSLTTPRPEDHGTNLTCQMK-ROGAQVTTERTVQLNVSYADQITIF- 242
 QY 294 SQANRTVLENLGNTSLPVLEGQSLCLVCVTHSSPPARLSWTQGVLSQSPDPGVLE 353
 DB 243 - - - - - RNLGIALEILQNTSVLPVLEGALRLCDAPNPFALHSWFGSPALNATPISNTGILE 300
 QY 354 LPRVQVEHEGEPTCHARHPVLSQVHVSLSVHYSPKLLGPSCSWAEGLHCSCSSQASPA 413
 DB 301 LRRVRSABEGGFTCRAGHPGLQIFLNLVSVGLPQLLPSCSWAEGLHCRCSPFARPA 360
 QY 414 PSLRWMLGELLNCSODSFVTPPSAGPWANSLSLHGLSSGLRCLRCEANVHGAQS 473
 DB 361 PSLCWRLEKPLEGNSQSGFKVNSSAGPWANSLSLHGLSSDLKVKSKANNVIGSQS 420
 QY 474 GSIIQLPKKGLISTAFNSGAFLIGITALLFLCLALIMKILPKRQTQETPRFRSRH 533
 DB 421 GSVLLQGRSNL- GTGVVPAALGGAGVWALLCICLIFFLIVKARKQA- AGRPEKMD 478
 QY 534 STLDYINVVPTAGPLAOKNOKATPNSRTPV- PPGAPSPESKKNQKQYQLPSPEPK 592
 DB 479 ED- - - - - PIMGTTTSGRKKPWPDPGDSQSPGDAPP- - - - - 511
 QY 593 SSTQAPESQESBELHYATNFPQVPRPRPEARMKGTQA- - - - - DYAEVK 637
 DB 512 - - - - - LEEQKELHYASISFSEMK- - - - - SREPKQEA PSTTEYSEIK 548
 RESULT 9

AAH29896
ID AAH29896 PRELIMINARY; PRT; 551 AA.
AC AAH29896;
DT 02-MAR-2004 (TRENDELrel. 27, Created)
DT 02-MAR-2004 (TRENDELrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENDELrel. 27, Last annotation update)
DE Sialic acid binding Ig-like lectin 5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Krausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bhat N.K., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Krausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029896; AAH29896.1; -
KW Lectin
SQ SEQUENCE 551 AA; 6068 MW; 65EA2B6B29B59304 CRC64;
Query Match 30.8%; Score 1039; DB 2; Length 551;
Best Local Similarity 39.3%; Pred. No. 2.1e-57;
Matches 255; Conservative 76; Mismatches 204; Indels 114; Gaps 15;
QY 2 LPLLLSLL-CGSOAMGDFWIRVOESVMVPEGLCISVPCSFSPRODWTGCTPAYGYW 60
DB 1 MLPLLLPLLLGGSLQKXPVLEQVQKSVTVQEGLCVLVPCSFSPWRSYSSPPLYVW 60
QY 61 FRAVTEETTKGAPVATNHQSREVMETGRFQLTGDPKXGNSLVLRDAQMODESOYFFRV 120
DB 61 FRDGEIPYVAEVVATNPNDRVKPSTQGRFLRGDVKXKNSLSIGDARMEDTGSYFFRV 120
QY 121 ERGSVYRNFMNDGFLKVTLSFTFRPDQNDTLTCHVDFSRKGVSAQRTVRLAVAP 180
DB 121 ERGRDVKYSYQOKNLEVTAL----- 142
QY 181 RDLVTSISRDNTFALPEPOGPNVPLEAKGQFRLLC-----AASQPPATLLSWVLQNRV 236
DB 143 -----LEKPDHFLFEP-----LESGRPTRLSLGSCAGPLFTFSWT--GNA 184
QY 237 LSSHPWGPRLGLGLPGVKAQDSGRYTCRAENRLGSG---ORALDLSVQVPPENLVMV 293
DB 185 LSPFLDPEATRSELTLTPRPEHGNLTQCMK-RQCAQVTTERTVQLNVSAQPTITIF- 242
QY 294 SQANRTVLENLNGSLPLVLEQSSCLVCTHSSPPARLSWTORQVLSPQSPDPGVLE 353
DB 243 --RNGIALEILQNTSVLPVLEQARLLCDAPSNPFAHLSWFGQSPALNATPISNTGLE 300
QY 354 LPRVQVEHEGEFTCHARHPLGSGVHVSLSVSHVSPKLLGSPCSWEAEGHLHCSCSQASPA 413

DB 301 LRRVSAEGGFTCRAQHPLGFLQIFLNLSVYSLPQLLGPCSCWEAEGHLHCSCSPRPA 360
QY 414 PSRLWMLGEBELLEGSSQSQSFVTPSSAGPFWANSSILHGLSSGLRLCRCEANVHGAQS 473
DB 361 PSCLWRLEEKPLEGSSQSQSFVKYNSSAGPFWANSSILHGLSSGLRLCRCKVSKAWNIYGSQS 420
QY 474 GSILQLPDKKGLISTAFSNGAPLIGIGITALLFLCLALIMKILPKRTOTETPRPRFSRH 533
DB 421 GSVLLQGRSNL-GTGVVPAALGGAGVALLCICLIFLIYVAKRKQA-AGRPKMWDD 478
QY 534 STILDYINVVPTAGPLAQKRNKATNSPTPL-PPGAPSPESKKNQKQYQLPSPPEPK 592
DB 479 ED-----PINGTITSGSRKPEWPSDAGDQASPPGDAPP----- 511
QY 593 SSTQAPESQESQELHYATLNFVGRPRPEARMKGTQA-----DYAEVK 637
DB 512 -----LEEQKELHYASLSFSEMK-----SREPKQCEAPSTTEYSEIK 548
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ID -SILF_MOUSE STANDARD; PRT; 569 AA.
AC Q920G3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin-F precursor (mSiglec-F).
GN Name=SiglecF; (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21576254; PubMed=11579105; DOI=10.1074/jbc.M108573200;
RA Angata T., Hingorani R., Varki N.M., Varki A.;
RT "Cloning and characterization of a novel mouse Siglec, mSiglec-F:
differential evolution of the mouse and human (CD33) Siglec-3-related
gene clusters.";
RL J. Biol. Chem. 276:45128-45136(2001).
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
dependent binding to cells. Preferentially binds to alpha2,3-
linked sialic acid. The sialic acid recognition site may be masked
by cis interactions with sialic acids on the same cell surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed by immature
monocytic/myeloid lineage cells in bone marrow. Also found at
lower levels in mature neutrophils and monocytes.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
motif is involved in modulation of cellular responses. The
phosphorylated ITIM motif can bind the SH2 domain of several SH2-
containing phosphatases.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
(sialic acid binding Ig-like lectin) family C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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DR EMBL; AF293371; AAL11043.1; -
DR HSSP; Q9Y286; 107S.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 2.

[illegible]

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Db 348 SRAPAPSLRWLGEVLEGNSTVTKSSAGQWANSLLLSMFPSNHRLSCEAW 407
Qy 467 NVHGAQSSIIQLPKKGLISTAFSN-----GAFLGIGITALLFLICLALII--MKIL 516
Db 408 SDNRVQRTATILLVSGPK--VSQAGKSESRGTGLGAIWAGLWALLAVCLCLIFFTKVL 465
Qy 517 PKR 519
Db 466 RKX 468

RESULT 12
SIL8 HUMAN
ID SIL8 HUMAN STANDARD; PRT; 499 AA.
AC Q9NYZ4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sialic acid binding Ig-like lectin 8 precursor (Siglec-8)
DE (Sialoadhesin family member-2) (SAF-2).
GN Name=SIGLEC8; Synonyms=SAF2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20549027; PubMed=11095983; DOI=10.1006/bbrc.2000.3866;
RA Fousias G., Yousef G.M., Diamandis E.P.;
RT "Molecular characterization of a siglec8 variant containing
RT cytoplasmic tyrosine-based motifs, and mapping of the siglec8 gene.";
RL Biochem. Biophys. Res. Commun. 278:775-781(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20314554; PubMed=10856141;
RA Kikly K.K., Bochner B.S., Freeman S.D., Tan K.B., Gallagher K.T.,
RA D'Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller C.L.,
RA Murdoch P.R., Tachimoto H., Schleimer R.P., White J.R.;
RT "Identification of SAF-2, a novel siglec expressed on eosinophils,
RT mast cells, and basophils.";
RL J. Allergy Clin. Immunol. 105:1093-1100(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=20092847; PubMed=10625619;
RA Floyd H., Ni J., Cornish A.L., Zeng Z., Liu D., Carter K.C., Steel J.,
RA Crocker P.R.;
RT "Siglec-8, A novel eosinophil-specific member of the immunoglobulin
RT superfamily.";
RL J. Biol. Chem. 275:861-866(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Floyd H., Zhang J.Q., Crocker P.R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC dependent binding to cells. Preferentially binds to alpha2,3-
CC linked sialic acid. Also binds to alpha2,6-linked sialic acid. The
CC sialic acid recognition site may be masked by cis interactions
CC with sialic acids on the same cell surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1; Synonyms=Long;
CC IsoId=Q9NYZ4-1; Sequences=Displayed;
CC Name=2;
CC IsoId=Q9NYZ4-2; Sequence=VSP_002559;
CC Name=3;
CC IsoId=Q9NYZ4-3; Sequence=VSP_002560;
CC -!- TISSUE SPECIFICITY: Expressed specifically on eosinophils.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
CC as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
CC motif is involved in modulation of cellular responses. The
```

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CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC containing phosphatases.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC
CC EMBL; AF287892; AAC00573.1; -
CC EMBL; AF223403; AAF34702.1; -
CC EMBL; AF195092; AAF27622.1; -
CC EMBL; AF310234; AAK55140.1; -
CC HSP; Q9Y286; 107S.
CC Genew; HGNC:10877; SIGLEC8.
CC MIM; 605639; -
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0005229; F:sugar binding; TAS.
CC GO; GO:0004888; F:transmembrane receptor activity; TAS.
CC GO; GO:0007165; F:signal transduction; TAS.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; Ig_2.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS00835; IG_LIKE; 2.
CC Alternative splicing; Cell adhesion; Glycoprotein;
CC Immunoglobulin domain; Lectin; Repeat; Signal; Transmembrane.
FT SIGNAL 1 16
FT CHAIN 17 499
FT DOMAIN 17 363
FT TRANSMEM 364 384
FT DOMAIN 385 499
FT DOMAIN 40 123
FT DOMAIN 157 240
FT DOMAIN 246 344
FT SITE 445 450
FT SITE 468 473
FT DISULFID 42 181
FT DISULFID 47 107
FT DISULFID 175 224
FT DISULFID 283 328
FT CARBOHYD 172 172
FT CARBOHYD 249 249
FT CARBOHYD 267 267
FT VARSPLIC 152 245
FT VARSPLIC 416 499
FT VARSPLIC 499 AA; 54042 MW; 086BFF989B74123C CRC64;
SQ SEQUENCE 499 AA; 54042 MW; 086BFF989B74123C CRC64;
Query Match 21.4%; Score 721.5; DB 1; Length 499;
Best Local Similarity 30.8%; Pred. No. 2,le-37;
Matches 207; Conservative 80; Mismatches 152; Indels 233; Gaps 21;
Qy 1 MLLPLLSSLLGGSQAVDG-----RFWIRVQSVVMVPEGLCLSVPCSFYPRQDWTGST 54
Db 1 MLLLLALLPLLLWGTGKMGEDRQYCDGYLLQVGLVTVQEGLCVHVPCSFYPRQDWTGSD 60
Qy 55 PAYGYWFKAVTEITKGAIPVATNHQSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDES 114
Db 61 PVGFWPFRADRPYQDAPVAINAPDREVAETQGRFQLLGDIWNSDCSLIRAKRKDG 120
Qy 115 QYFFRVERGSYRNFNMNDGFF----LKVTLSFTPRP-----QDHTDLTCHVDV 161
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Q96PQ1; Q8IYH7;
 28-FEB-2003 (Rel. 41, Created)
 28-FEB-2003 (Rel. 41, Last sequence update)
 01-OCT-2004 (Rel. 45, Last annotation update)
 Sialic acid binding Ig-like lectin-like 1 precursor (Siglec-like molecule 1) (Siglec-L1) (UNQ9215/PRO34042).
 Name=SIGLECL1; Synonyms=SLG;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
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 SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 TISSUE=Bone marrow;
 MEDLINE=21303046; PubMed=11409877; DOI=10.1006/dbrc.2001.5052;
 Fousias G., Taylor S.M., Yousef G.M., Tropak M.B., Ordon M.H.,
 Diamandis E.P.;
 "Cloning and molecular characterization of two splice variants of a
 new putative member of the Siglec-3-like subgroup of Siglecs.";
 RL Biochem. Biophys. Res. Commun. 284:887-899(2001).
 [2]
 SEQUENCE FROM N.A. (ISOFORM LONG).
 MEDLINE=21523976; PubMed=13546777; DOI=10.1074/jbc.M105926200;
 Angata T., Varki N.M., Varki A.;
 "A second uniquely human mutation affecting sialic acid biology.";
 RL J. Biol. Chem. 276:40282-40287(2001).
 [3]
 SEQUENCE FROM N.A. (ISOFORM LONG).
 MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
 Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 Godowski P., Gray A.;
 "The secreted protein discovery initiative (SPDI), a large-scale
 effort to identify novel human secreted and transmembrane proteins: a
 bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 [4]
 SEQUENCE FROM N.A. (ISOFORM LONG).
 TISSUE=Blood;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
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 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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 Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalley D.E.,
 Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
 dependent binding to cells. The sialic acid recognition site may
 be masked by cis interactions with sialic acids on the same cell
 surface.
 CC -!- ALTERNATIVE PRODUCTS:
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- Event=Alternative splicing; Named isoforms=2;

Name=Long; Synonyms=SLG-L;
 IsoId=Q96PQ1-1; Sequence=Displayed;
 Name=Short; Synonyms=SLG-S;
 IsoId=Q96PQ1-2; Sequence=VSP_002566;
 -!- TISSUE SPECIFICITY: The short isoform is highly expressed in
 spleen, small intestine and adrenal gland; it is lower expressed
 in thyroid, placenta, brain, stomach, bone marrow, spinal chord and
 testis. The long isoform is highly expressed in spleen, small
 intestine and bone marrow; it is lower expressed in thyroid,
 placenta, thymus, trachea, stomach, lung, adrenal gland, fetal
 brain and testis.
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to
 as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This
 motif is involved in modulation of cellular responses. The
 phosphorylated ITIM motif can bind the SH2 domain of several SH2-
 containing phosphatases.
 CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
 (sialic acid binding Ig-like lectin) family C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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 CC -----
 EMBL; AF277806; AAK51233.1; -;
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 EMBL; AF282256; AAK71521.1; -;
 EMBL; AY358140; AAQ88507.1; -;
 EMBL; BC035809; AAH35809.2; -;
 HSP; Q9Y286; 107S.
 Genew; HGNC:15482; SIGLECL1.
 MIM; 606094; -;
 InterPro; IPR007110; Ig-like.
 Pram; PF00047; Ig; 4.
 PROSITE; PS00835; IG_LIKE; 3.
 KW Alternative splicing; Cell adhesion; Glycoprotein;
 KW Immunoglobulin domain; Lectin; Polymorphism; Repeat; Signal;
 KW Transmembrane.
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 FT CHAIN 19 595 Sialic acid binding Ig-like lectin-like
 FT 1.
 FT DOMAIN 19 481 Extracellular (Potential).
 FT TRANSMEM 482 502 Potential.
 FT DOMAIN 503 595 Cytoplasmic (Potential).
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 FT DOMAIN 143 269 Ig-like V-type 2.
 FT DOMAIN 275 358 Ig-like C2-type 1.
 FT DOMAIN 365 462 Ig-like C2-type 2.
 FT SITE 563 568 ITIM motif.
 FT SITE 586 591 SLAM-LIKE MOTIF.
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 FT DISULFID 166 299 By similarity.
 FT DISULFID 171 231 By similarity.
 FT DISULFID 293 342 By similarity.
 FT DISULFID 401 446 By similarity.
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 FT CARBOHYD 360 360 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 367 367 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
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 (in isoform Short).
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:18 ; Search time 21.6516 Seconds
(without alignments)
1957.231 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377
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Scoring table: BLOSUM62
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1033	30.6	551	4	US-08-896-537A-2
2	774.5	22.9	421	3	US-08-759-628-5
3	667.5	19.8	431	3	US-09-038-832-2
4	667.5	19.8	431	3	US-09-038-832-4
5	626	18.5	467	3	US-09-046-736-2
6	586.5	17.4	440	3	US-08-759-628-4
7	532.5	15.8	374	3	US-09-046-736-4
8	448.5	13.3	364	4	US-08-896-537A-3
9	237.5	7.0	318	6	5242798-5
10	230.5	6.8	501	2	US-08-408-095-31
11	229	6.8	917	1	US-08-245-295-2
12	229	6.8	917	1	US-08-481-130-2
13	229	6.8	917	1	US-08-656-984A-2
14	229	6.8	917	2	US-08-485-604-2
15	229	6.8	917	2	US-08-487-595-2
16	228.5	6.8	924	1	US-08-481-130-28
17	228.5	6.8	924	1	US-08-656-984A-28
18	228.5	6.8	924	1	US-08-485-604-28
19	228.5	6.8	924	2	US-08-487-595-28
20	225	6.7	1241	3	US-09-040-774-2
21	217.5	6.4	1070	4	US-09-961-403-3
22	214	6.3	607	2	US-08-752-307B-12
23	214	6.3	607	3	US-09-707-802-12
24	214	6.3	607	3	US-09-991-326-12
25	206	6.1	464	2	US-08-602-725-32
26	200.5	5.9	642	1	US-08-217-299-1
27	200.5	5.9	698	2	US-08-602-725-36

28	200.5	5.9	734	2	US-08-389-459A-17	Sequence 17, Appl
29	200.5	5.9	734	3	US-08-987-867A-17	Sequence 17, Appl
30	200	5.9	56	4	US-09-513-999C-4599	Sequence 4599, Ap
31	199.5	5.9	1953	4	US-09-917-254-92	Sequence 92, Appl
32	197.5	5.8	280	4	US-09-270-767-43068	Sequence 43068, A
33	194	5.7	828	1	US-08-261-304-2	Sequence 2, Appl
34	193.5	5.7	1209	4	US-09-130-158A-2	Sequence 2, Appl
35	192.5	5.7	424	6	PCT-US95-08493-13	Patent No. 5169835
36	191.5	5.7	946	5	US-09-383-586-31	Sequence 13, Appl
37	191	5.7	529	3	US-09-823-038A-31	Sequence 31, Appl
38	191	5.7	529	4	US-08-752-307B-14	Sequence 14, Appl
39	188.5	5.6	630	2	US-09-707-802-14	Sequence 14, Appl
40	188.5	5.6	630	3	US-09-991-326-14	Sequence 14, Appl
41	188.5	5.6	630	3	US-08-986-485-5	Sequence 5, Appl
42	188	5.6	1091	3	US-08-752-307B-11	Sequence 11, Appl
43	187.5	5.6	612	2	US-09-707-802-11	Sequence 11, Appl
44	187.5	5.6	612	3	US-09-991-326-11	Sequence 11, Appl
45	187.5	5.6	612	3	US-09-991-326-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-896-537A-2
; Sequence 2, Application US/08896537A
; Patent No. 6590088
; GENERAL INFORMATION:
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Rosen, Craig A.
; FILE REFERENCE: CD33-Like Protein
; TITLE OF INVENTION: CD33-Like Protein
; CURRENT APPLICATION NUMBER: US/08/896,537A
; CURRENT FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,481
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-896-537A-2

Query March		30.6%	Score 1033;	DB 4;	Length 551;
Best Local Similarity		39.0%	Pred. No. 4.7e-80;		
Matches 253;		Conservative 78;	Mismatches 204;	Indels 114;	Gaps 15;
Qy	2	LLPILLSLL-GGSOAMDGRFWIRVQBSVMVPEGLICISVFCSPYPRQDWTGSTPAYGYW	60		
Db	1	MLPILLSLL-GGSOAMDGRFWIRVQBSVMVPEGLICISVFCSPYPRQDWTGSTPAYGYW	60		
Qy	61	FKAVTETTKGAPVATNHQSRREVMSTGRFQLTGDPKAGNCSLVIRDAQVDSQYFFRV	120		
Db	61	FRDGEIPIYAEVATNPNDRVRKPTQGRFRLIGDVQKNCSLSIGDARMEDTGSYFFRV	120		
Qy	121	ERGSYVYNNMDGFFLKVTLSFTPEPDHNDLTCHVDFSRKGVSAQTVRLRVAYAP	180		
Db	121	ERGRDVKISYQCKKINLEVTAL	142		
Qy	181	RDVLVISRDNTPALEPQGNVPEYLEAKGQFLRLC----	236		
Db	143	-----LESGRPTLLCSLPFGSCGAGPLTFTSWT--GNA	184		
Qy	237	LSSHPHNGPPLGLGLPGVKGAGSGRYTCRAENRLSQ----	293		
Db	185	LSPDPTTTSSELTLPREDHGTNTLCQMK-RQGAQVTTERTVQLNVSPQTITF-	242		
Qy	294	SOANRTVLENLNGTSLPVLGQSCLVVCVTHSSPPARLSWTQRGVLSQSDPGVLE	353		
Db	243	--RNGIALEILQNTSYLPVLEGGQALRLCCAPSNPPAHLNFWFGSPALNATPISNTGILE	300		

354 LPRVQVHEGEFTCHARHPLGSHVLSLSVHYPKLLQPSCSWEAEGHLCSSQASPA 413
301 LRRVSAEXGGFTCAQHPLGFLQIFLNLVSVSLPQLLQPSCSWEAEGHLCRCSPAWPA 360
414 PSLRWLGELELGNSSQDSFEVTPSSAGPWNSSLSLHGLSSGLRLCEAWNVHGAOS 473
361 PSLRWLGELELGNSSQDSFEVTPSSAGPWNSSLSLHGLSSGLRLCEAWNVHGAOS 420
474 GSILQLPDKKXGLISTAFNGAFIGITALLFICLALIMKILPKRRTQTETPRFRSRH 533
421 GSVLLQLGRSNL-GTGVVPAALGGAGVALLCICLCLIFLIVKARRKQA-AGREPKXDD 478
534 STILDVINVVTPAGPLAQKRNQKATNSPRTL-PRGAPSPESKKNQKQYQLPSPPEPK 592
479 ED-----PINGTITTSRKKPWPDPDQASPGDAPP----- 511
593 SSTQAPESQESBELHYATLNTFPGVPRPEARMKGTQA-----DYAEVK 637
512 -----LEEKELHYASLSFSEMK-----SREPKDQEAPOSTTEYSEIK 548

RESULT 2

US-08-759-628-5
Sequence 5, Application US/08759628
Patent No. 6225446

GENERAL INFORMATION:

APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 03-DEC-1996

CLASSIFICATION:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574

FILING DATE:

FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.

REGISTRATION NUMBER:

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q

TELEPHONE:

TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO:

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid

STRANDEDNESS:

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-759-628-5

Query Match

Best Local Similarity 22.9%; Score 774.5; DB 3; Length 421;

Matches 186; Conservative 49; Mismatches 146; Indels 71; Gaps 9;

3 LPLLLSSLL-GGSQAMGDFWIRQESVNVMPGLGICISVPCSPSYPRQDWTGSTPAYGYWF 61

Db 1 MELLPLLLGGSLQEKPVYELQVQSVTVQEGLCVLVPCSFYWRWSVSSPLYYVWF 60
QY 62 KAVTETTKGAPVATNHQREVEMSTRGRFOLTGDPKAGKNSLVIRDAQMODSQQYFFRVE 121
Db 61 RDGEIPYVAEVAATNPDRAVKETQGRFELLGQVQKNCNLSIGDARMEDTGSYFFRVE 120
QY 122 RGSVVRNFMNDGFFLKVTVLSTFPRQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAPR 181
Db 121 RGRDVKYSYQONKLNLEVTALIEKP-----DIHLSP----- 152
QY 182 DLVISISRDNTPALEPQPGNVPLVLEAKGQFLRLCAADSQ-----PPATLSWVLQNRVL 237
Db 153 -----LESGLWRPTRLSCSLPGSCVAGPPLTFTSGN----- 184
QY 238 SSSHPWGPRLG---LELPGVKAGDSGRYTCRAENRLGSO---ORALDLSVQYPPENLRV 291
Db 185 AXSAPMTPRXPAPRELTLTPRPEDHGTNLTCOMK-RGAQVTTXTVQLNVSYAPQTITI 243
QY 292 MVSOANETVLENLNGTSLPVLGQSILCVVTHSSPPARLSWTRQGVLSPSQSDPGV 351
Db 244 F---RNGIALEILQNTSYLPVLEQQAIRLLCDAPSPPAHLSPQSPALNATPISNTGI 300
QY 352 LELPRVQVHEGEFTCHARHPLGSHVLSLSVHYPKLLQPSCSWEAEGHLCSSQAS 411
Db 301 LELRRVSAEXGGFTCAQHPLGFLQIFLNLVSVSLPQLLQPSCSWEAEGHLCRCSPAR 360
QY 412 PPSLRWLGEELELGNSSQDSFEVTPSSAGP 443
Db 361 PPSLRWLGEELELGNSSQDSFEVTPSSAGP 392

RESULT 3

US-09-038-832-2

Sequence 2, Application US/09038832

Patent No. 6146845

GENERAL INFORMATION:

APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-2
TITLE OF INVENTION: (SAF-2)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINIER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,886
FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SEQ ID NO:

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-038-832-2

Query Match      19.8%; Score 667.5; DB 3; Length 431;
Best Local Similarity 39.2%; Pred. No. 7.9e-49;
Matches 162; Conservative 52; Mismatches 102; Indels 97; Gaps 10;

QY 1 MLLPILLSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSPRODWTGST 54
DB 1 MLLLLLLLLPWLWGTGKMGDRQYGDGYLLQVQLVTVQEGLCVHVPCSFSPQDGTSD 60
QY 55 PAYGWFWKAVTETTKGAPVATNHQREVMSTGRFQLTGDPKAGNCSLVIRDAQMDES 114
DB 61 PVHGWFYFRAGDRPYQDAPVATNPDREVQAEQGRFQLLGIWNSDCSLSDARKKDKG 120
QY 115 QYFRRVERGSVRYNFMNDGPE---LKVTVLSFTPRP-----QDHTDLTCHVDF 161
DB 121 SYFFRLERGS-MKWSYKSQLNYKTQLSVFTALTHTRPDILLGLTSGHSENITCSVPW 179
QY 162 SRK-----GVSQRTVRLRVAYAPRDLVISISRDNTPALEPQPGNVVYLEAQKG 211
DB 180 ACKQGTPTMISIGASVS-----SPGP---TTARSSVLTLPKPDHGTSLTCQ-- 225
QY 212 QFLRLCADSQPPATLSWVLQNRVLSSHPWGPRLGLELPGVKAGDSGRYTCRAENRL 271
DB 226 -----VTLPG--TGVTTTSTVR----- 240
QY 272 GSQORALDLSCVYPENLRVWVSQANRTVLENLNGTSLPVLGQSLCLVCVTHSSPPAR 331
DB 241 -----LDVSYPPNLTMTVFGDATASTALNGSSLSVLEQSLALVCVNSNPPAR 292
QY 332 LSWTORGQVLSQSPDQGVLELPRVQVEHEGEFTCHARHPLGSOHVLSLSV 384
DB 293 LSWTRGSLTLCPSRSSNFGLELPRVHVHVRDEGEFTCRAQNAQGSQHLSLSL 345

RESULT 4
US-09-038-832-4
; Sequence 4, Application US/09038832
; Patent No. 6146845
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-2
; TITLE OF INVENTION: (SAF-2)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 11-MAR-1998
; CLASSIFICATION:
; APPLICATION NUMBER: 60/041,886
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
```

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; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 431 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-038-832-4

Query Match      19.8%; Score 667.5; DB 3; Length 431;
Best Local Similarity 39.2%; Pred. No. 7.9e-49;
Matches 162; Conservative 52; Mismatches 102; Indels 97; Gaps 10;

QY 1 MLLPILLSLLGGSQAMDG-----RFWIRVQESVMVPEGLCISVPCSFSPRODWTGST 54
DB 1 MLLLLLLLLPWLWGTGKMGDRQYGDGYLLQVQLVTVQEGLCVHVPCSFSPQDGTSD 60
QY 55 PAYGWFWKAVTETTKGAPVATNHQREVMSTGRFQLTGDPKAGNCSLVIRDAQMDES 114
DB 61 PVHGWFYFRAGDRPYQDAPVATNPDREVQAEQGRFQLLGIWNSDCSLSDARKKDKG 120
QY 115 QYFRRVERGSVRYNFMNDGPE---LKVTVLSFTPRP-----QDHTDLTCHVDF 161
DB 121 SYFFRLERGS-MKWSYKSQLNYKTQLSVFTALTHTRPDILLGLTSGHSENITCSVPW 179
QY 162 SRK-----GVSQRTVRLRVAYAPRDLVISISRDNTPALEPQPGNVVYLEAQKG 211
DB 180 ACKQGTPTMISIGASVS-----SPGP---TTARSSVLTLPKPDHGTSLTCQ-- 225
QY 212 QFLRLCADSQPPATLSWVLQNRVLSSHPWGPRLGLELPGVKAGDSGRYTCRAENRL 271
DB 226 -----VTLPG--TGVTTTSTVR----- 240
QY 272 GSQORALDLSCVYPENLRVWVSQANRTVLENLNGTSLPVLGQSLCLVCVTHSSPPAR 331
DB 241 -----LDVSYPPNLTMTVFGDATASTALNGSSLSVLEQSLALVCVNSNPPAR 292
QY 332 LSWTORGQVLSQSPDQGVLELPRVQVEHEGEFTCHARHPLGSOHVLSLSV 384
DB 293 LSWTRGSLTLCPSRSSNFGLELPRVHVHVRDEGEFTCRAQNAQGSQHLSLSL 345

RESULT 5
US-09-046-736-2
; Sequence 2, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-MAR-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
```

REGISTRATION NUMBER: 23,031
 REFERENCE/DOCKET NUMBER: GH-50019
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-407-0700
 TELEFAX: 610-407-0701
 TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 467 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-046-736-2

Query Match 18.5%; Score 626; DB 3; Length 467;
 Best Local Similarity 28.6%; Pred. No. 3.3e-45;
 Matches 186; Conservative 79; Mismatches 184; Indels 202; Gaps 15;

Qy 2 LLPLLSSLLGGQAMGR-----FWIRVQSVWVPEGLCTSVPCSPSYPRQDWTGSTP 55
 Db 1 MLLLLLLLWGRVEGQKRNKDYSLTWQSSVTQEGMCVHVRCSPSYPVDSQTSDDP 60
 Qy 56 AYGWFKAVTETTKGAPVATNHOSREVENSTGRFOLTGDPKAGNCSLVIRDAQMDQDSQ 115
 Db 61 VHCYWFAGNDISWKAFAVATNPAWAVQETDRFHLGDPQTKNCTLSIRDAQMDAGR 120
 Qy 116 YPRVRSYVRYNFMNDGFFKVTVLSTPQDHT-----DLTCHVDPSRKGVSA 168
 Db 121 YFRMEKGN-IKNWYKDYQLSVNVTALTRPNILIPGTLESQFQNLTCVSWACEQGT 179
 Qy 169 QRTVRLRVAVAPRDLVISRNTTPALEPQPGQNVPLYEAQKGQFLRLCAADSOPTAL 228
 Db 180 PWISWMTGSVDPH--PSTRGSVLTLIPQOHGTSLTGQ----- 218
 Qy 229 SWVLQNRVLSHGHMGPRLGLELFCVKAGDSGRYTCRAENRLGSGQQRALDLSVQYPP 288
 Db 219 -----VTLPGAGV-----ITNRTIQLNVSYPPQN 242
 Qy 289 LRVWNSQANRTVLNGLNGTSLPVLEGQSLCLVCVTHSSPPARLSWTORGQVLSQSPSD 348
 Db 243 LTVTFQGGEGTASTALGNSSLSVLEGQSLRLVCAVDSNPPARLSWTWRSLSLTPSPQSN 302
 Qy 349 PGVLELPRVQVEHEGFTCHAHPLGSGHVSLSV--HYSKLLGPSCSWEAEGHLCSC 406
 Db 303 PLVLEL-QVHLGDEGFTCEAQNLSGSHVSLNLSLQOEYTGK----- 345
 Qy 407 SSCASPAPSLRWLWGLLEGNSQDSFEVTPSSAGPWANSLSLHGGLSGLRLURCEAW 466
 Db 346 ----RPV----- 348
 Qy 467 NVHGAQSGSILQIPDKKGLISTAFSNGAPLIGITALLFLCLALIMKILPKRTQETP 526
 Db 349 -----SGVLL-----GAVGGAGATLVFLSPCVFIWV---RSCRKXSA 384
 Qy 527 RPFGRHSTILDYINVVPTAGLAQKRNQKATPNSPRTPLPGAPSPSKNKKQYQLP 586
 Db 385 RP-----AADVDGVGMK-----DANTIRGSASQGNLTESW 414
 Qy 587 SPFEPKSSSTQAPESQESQELHYATLNFVGRPRPEARMKGTQADYAEVK 637
 Db 415 AADNPRHHGLAAHSSGEEREIQYAPLSFKXGEPQ-DLSGQCATNNEYSEIK 464

RESULT 6

US-08-759-628-4

Sequence 4, Application US/08759628

Patent No. 6225446

GENERAL INFORMATION:

APPLICANT: Altman, Scott W.

APPLICANT: Rock, Fernando L.

APPLICANT: Bazan, J. Fernando

APPLICANT: Kastelein, Robert A.

TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DNAX Research Institute
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/759,628
 FILING DATE: 05-DEC-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/008,574
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ching, Edwin P.
 REGISTRATION NUMBER: 34,090
 REFERENCE/DOCKET NUMBER: DX0552Q
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-852-9196
 TELEFAX: 415-496-1200
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 440 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-759-628-4

Query Match 17.4%; Score 586.5; DB 3; Length 440;

Best Local Similarity 24.7%; Pred. No. 7.4e-42;

Matches 172; Conservative 73; Mismatches 133; Indels 317; Gaps 15;

Qy 2 LLPLLSSLLGGQAMGRFWIRVQSVWVPEGLCTSVPCSP--SYPRQDWTGSTPAYGY 59

Db 1 MLPLLPFWLWAGLAQERRPQEGESLTVQEGLCVLPCLPTTLP-----ASYVGYGY 55

Qy 60 WFKAVTETTKGA--PVATNHOSREVENSTGRFOLTGDPKAGNCSLVIRDAQMDQDSQYF 117

Db 56 WF-----LEGADVATNDPDEEVQETGRPHLLWDPKRNCSLSIRDARRDNAAVF 109

Qy 118 FRVERGSYVRYNFMNDGFFLKV----- 139

Db 110 FRL-KSKWKYGYTSSKIVYRVWVVALTRPMISIPGVPWSSNLTCSVPWVCEQGTPIF 168

Qy 140 -----TVLSFTPRPDQDHTDLTCHVDPSRKGVSAQRTVRLRVAVAPRD 182

Db 169 SWSMAAPHLGLPRITTSVLTITP-AQDHSNTLTCQVTFPGAVTMTERTIQLNVSAPOK 227

Qy 183 LVTSISRDNTPALPEPQPGQNVPLYEAQKGQFLRLCAADSOPTALSWVLQNRVLSSSH 242

Db 228 VASIQGNSAEPK-----ILQNT----- 246

Qy 243 WGPRLGLELPGVKAGDSGRYTCRAENRLGSGQQRALDLSVQYPPENLRVWNSQANVTLE 302

Db 247 ----- 246

Qy 303 NLNGTSLPVLEGQSLCLVCVTHSSPPARLSMTORGQVLSQSPSPGVLELPRVQVHEH 362

Db 247 -----SSLPVLEGQALRLCLDADGNPFAHLSWFQASPPNATPISNTGVLELPQVGSASE 301

Qy 363 GETTCHARHPLGSGHVSLSVSPKLLGSPCSWEAEGHLCSCSSQASPAFSLRWLWGE 422

Db 302 GDFTCRAQHPGLSGLSLSLFVH-----WKPEG----- 329

QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRCEANNVHGAQSGSILQLPDK 482
Db 330 -----RAGGVL----- 335
QY 483 KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTOTETPRPFSRSTILDYINV 542
Db 336 -----GAVGASITTLVFLCVCFIF-----RVKTRKKQPSOCKYTDVNP 376
QY 543 VETAGLAQRNKAQKATPNSPRTPLPPGAPSPESKKNQKQYQLPSPFPKSSSTQAPESQE 602
Db 377 VNVSG-----SRGHQHQFQTGIVSDHPAEPAGPISE 406
QY 603 SOEELHYATLNPFGVYRPRPEARMKPGTQADYAEVK 637
Db 407 DEQELHYAVLHPHKVQPOE-----PKVTDTEYSEIK 437

RESULT 7

US-09-046-736-4
; Sequence 4, Application US/09046736
; Patent No. 6090582
; GENERAL INFORMATION:
; APPLICANT: KIKLY, KRISTINE
; APPLICANT: ERICKSON-MILLER, CONNIE
; TITLE OF INVENTION: Sialoadhesin Family Member-3
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,736
; FILING DATE: 24-Mar-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/041,885
; FILING DATE: 02-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-046-736-4

Query Match 15.8%; Score 532.5; DB 3; Length 374;
Best Local Similarity 25.2%; Pred. No. 2.5e-37;
Matches 162; Conservative 64; Mismatches 137; Indels 281; Gaps 12;
QY 2 LPLLLLSLLGSGQANDGR-----FWIRVQBSVMYPEGICISVPCSFYPRQDWTGSP 55
Db 1 MLLLLLPULLWGRVERVEWOKNRKDYSLTMQSSVTVQEGNCVHVRCSFYPVDSQSDSP 60
QY 56 AYGYWFKAVTETTKGAPVATNHQSRVENMSTRGRFOLTGDPKAGNCSLVIRDAQMDESQ 115
Db 61 VHGWFYFRAGNDISWKAIPVATNFAVQBEETRDPRHLLGDPQTKNCTLSIRDARMSDAGR 120

QY 116 YFRVVRGSRVYRNFVNDGFFLKVTVLSFTPPQDHTDLTCHVDPSRKVSAQRTVRLR 175
Db 121 YFRMEKGN-IKNYKID----- 137
QY 176 VAVAPRDLVISIRDNTPALEPOQGNVPYLEAQKGQFLRLCAADSQPPATILSWVLQNR 235
Db 138 ----- 137
QY 236 VLSSHPWGPRLGLELPGVAGDSGRYTCRAENRLGSGQORALDLSVQYPPENLRVMVSQ 235
Db 138 -----QLSVNVTYPPQNLTVTVFQ 156
QY 296 ANRTVLNLTNGTSLPVLEGQSLCLCVTHSSHPPARLSMTQGVLSPSQSPDPGVLELP 355
Db 157 GEGTASTALGNSSLSVLEGQSLRLCAVDNSNPAPARLSWTWRSRLTLYPSQSPNPLVLEL- 215
QY 356 RVQVEHEGEFTCHARHPLGSHVLSLSV--HYSPKLLGPFSCSWEAEGHLCSSQASPA 413
Db 216 QVHLGDEGEFTCRAQNSLGSQHVSLNLSLQOEYTKM-----RPV 255
QY 414 PSLRWLGBELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRCEANNVHGAQS 473
Db 256 -----S 256
QY 474 GSILQLPDKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRTOTETPRPFSRH 533
Db 257 GVLL-----GAVGAGATALLVFLSFCVFIW--RSCRKKSARP----- 293
QY 534 STILDYINVVPTAGPLAQRNKAQKATPNSPRTPLPPGAPSPESKKNQKQYQLPSPFPKPS 593
Db 294 -----AADVGDIGMK-----DANTIRGASQGNLTESWADDNPRH 328
QY 594 STQAPESQESQELHYATLNPFGVYRPRPEARMKPGTQADYAEVK 637
Db 329 HGLAAHSGEEREIQYAPLSFHKGEPQ-DLSGQEAATNNEISEIK 371

RESULT 8

US-08-896-537A-3
; Sequence 3, Application US/08896537A
; Patent No. 6590088
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: CD33-Like Protein
; FILE REFERENCE: 1488.0480001
; CURRENT APPLICATION NUMBER: US/08/896,537A
; CURRENT FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 60/022,481
; PRIOR FILING DATE: 1996-07-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-896-537A-3

Query Match 13.3%; Score 448.5; DB 4; Length 364;

Best Local Similarity 21.4%; Pred. No. 3.9e-30;
Matches 149; Conservative 48; Mismatches 110; Indels 389; Gaps 11;
QY 1 MLLPLLLLSLLGSGQANDGRFWIRVQBSVMYPEGICISVPCSFYPRQDWTGSPAYGYW 60
Db 1 MPLLLLLPLWAGALAMPDPNFWLQVQBSVTVQEGLCVLVPCTFPHFPIPYDKNSPVEHYW 60
QY 61 PKAVETITKGAPVATNHQSRVENMSTRGRFOLTGDPKAGNCSLVIRDAQMDESQYFPRV 120
Db 61 FREGAIIISGDSFPAVINKLDQVEQBEETQGRFKLLGDPGRNNCSLIVDARRDNQSYFRM 120
QY 121 ERGSYVRVNFVNDGFFLKVTV----- 140

121 ERGS-TKYSKSPOLS-VHVDLTHRPKILIPGLTEPHSHKNLTCSVSWACEQTPPIPSM 179
141 -----VLSFTRPQDHTDLTCHVDFSRKGSQAQTVRLVAYAPRDIV 184
180 LSAAPTSLGRTHSSVLIITPRPQDHTNLTCQVKAQAGVTTERIGLVYYP----- 235
185 ISIRDNTPALPQPNVPLEAQKQGLRLILCAADSPAPFLSVLQNRVLSSSHWP 244
236 -----QNPIT----- 240
245 PRPLGLPQVACD-SGRYTCAENRLGSQLALDSVQPPENLRVMVQANRTVLEN 303
241 -----GIFPDGSGKQETRA----- 255
304 LGNGTSLPVLGQSLCLVCVTHSSPPARLSWTQGVLSQSPQSDPGVLELPRVQVEHEG 363
256 ----- 255
364 EFTCHARHPLGSHVLSLSVHVPKLLGSPCSWEAEGHLCSCSQASPAPSLRWLGE 423
256 ----- 255
424 LLEGNSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRLRCEAWNVHGAQSGSILQPKK 483
256 -----GL-----VHGA-GGA----- 265
484 GLISTAFSNGAPLGIGITALLFLCLALIMKILPKRTQTETPRPRFSRHSHTILDYINV 543
266 -----GVTALLALCLCLIFFIVKTHERRKAARTAVGSDNTHPT----- 302
544 PTAGPLAOKXKATNSRTPPLPQAPSDESKKQKQYQLPSPPEKSSSTQAPESQBS 603
303 -----TGSAPKQKQKSK-----LHGPTSTSCSGAAPTVM 334
604 QEBLHYATLNFQVRPRPBARPKGTQADYAEVKFQ 639
335 DEELHYASLNFHGMNP-----SKDTSTSEYSEVRTO 364

RESULT 9

3242798-5
Patent No. 5242798
APPLICANT: SUTCLIFFE, J. GERGO
TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES CORRESPONDING
TO PORTIONS OF PROTEINOIDS TRANSLATED FROM BRAIN-SPECIFIC MRNAs,
RECEPTORS, METHODS AND DIAGNOSTICS USING THE SAME
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
FILING DATE: 07-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 58,620
FILING DATE: 03-JUN-1987
APPLICATION NUMBER: 516,136
FILING DATE: 21-JUL-1983
SEQ ID NO: 5
LENGTH: 318

5242798-5

Query Match 7.0%; Score 237.5; DB 6; Length 318;
Best Local Similarity 25.1%; Pred. No. 4.2e-12;
Matches 95; Conservative 60; Mismatches 146; Indels 77; Gaps 13;
QY 272 GSGQALDLSVQYPPENLRVMVQANRTVLENLNGHTSLPVLGOSLGLCVCTHSSPPAR 331
DB 4 GQDNRVLSVMVYAPKPTV-----NGTVAV-EGETVILSTQSNPDPI 48
QY 332 LSWTQGVLSQSPQSDPGVLELPRVQVEHEGFTCHARHPLGSHVLSLSVHSPKLL 391
DB 49 LTIKFKQILATVIVESQLQLELPAVTPEDDGEYWCVAENQVQGRATAFNLSEVFAPIL 108
QY 392 GPS-CSWEAEGHLCSCSQASPAPSLRWLGLLEGNSSQDSFEVTPSSAGPWANSSLS 450

DB 109 LESHCAARDTVQCLVVKSNPPEVAFELPSRNVTNTEREP-VYSERSGLLLTSILT 167
QY 451 LHGGLSSGLRLRCEAWNVHGAQSGSILQPKKGLISTAFSNG-----AFLGIGITALLF 505
DB 168 LRGAQAPPRVICTSRNLVGTQS---LELP-----FGAHLNMWAKIGVGVAVAF 215
QY 506 LCLALIMKILPKRTQTETPRPRFSRHSHTILDYINVVPTAGPLAOKXKATNPSPRTP 565
DB 216 ALLIALVCYITQTRKKNVTESPSFS-----AG-----DNPHVL 249
QY 566 LPP-----GAPSP-ESKKNQKQYQLPSPPEKSSSTQAPESQSQEBLHYATLNFQVRP 619
DB 250 YSPFRISGAPDKYSEKRLGSERRLLGL-----RGEPELDLSYSHSDL-GKRP 298
QY 620 RPEARMPKGTQADYAEVK 637
DB 299 TKDSYTLTEELAEYAEIR 316

RESULT 10

US-08-408-095-31
Sequence 31, Application US/08408095
Patent No. 5856678
GENERAL INFORMATION:
APPLICANT: Chinnadurai, Govindaswamy
TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mack, Susan J.
REGISTRATION NUMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-408-095-31

Query Match 6.8%; Score 230.5; DB 2; Length 501;

Best Local Similarity 20.8%; Pred. No. 3.3e-11;
Matches 138; Conservative 66; Mismatches 219; Indels 239; Gaps 29;
QY 24 RVQESVMVPPGLGICISYPCSFSPYQDWTGTSTPAYGVFKAVTETT-----KGAPVAIN 76
DB 30 RTEKVHPIKIL-----PWHAGT-----YSCVAENILGTGORGGAELDVQ 70
QY 77 HQSREVEMSTRGRFQL-TGDPKNGNSLVIRDAQODESQYFRRVERGSYRVNFMNDGF 135
DB 71 YPPKKTVTIQNPMPIREGDVTVLSGN-----YNSNPSVTYEMKPHGA 115
QY 136 F-----LKVTVLSITPRPQDHTDLTCHVDFSRKGSQAQTVRLVAYAPRDIVIS 188
DB 116 WEPSGLVKLQNVGM-----DNTTIAC-----ARCNSWCNSWSPVALNVQYAPRDVVRKI 167

ZIP: 60606-6402
 COMPUTER READABLE FORM: disk
 MEDIUM TYPE: Floppy
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,130
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/827,689
 FILING DATE: 27-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/889,724
 FILING DATE: 26-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,061
 FILING DATE: 05-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/009,266
 FILING DATE: 22-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/102,852
 FILING DATE: 05-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/245,295
 FILING DATE: 18-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: WILLIAMS, JR. JOSEPH A.
 REGISTRATION NUMBER: 38,659
 REFERENCE/DOCKET NUMBER: 27866/32713
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 917 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-481-130-2

Query Match 6.8%; Score 229; DB 1; Length 917;
 Best Local Similarity 24.8%; Pred. No. 1.1e-10;
 Matches 112; Conservative 49; Mismatches 146; Indels 144; Gaps 22;
 QY 32 PEGLCISVPCSFYPRQDGTGTPAYGWFKAVTTTKGAPVATNHQSRVEMSTGRFQ 91
 DB 335 PEGKAVTVC-----WAGA-----RALV-TLEGIPAVPGQPAELQLN----- 371
 QY 92 LTGDFAKGNCSLVIRDAQMDQESQYFFRVERGSYYRNFMDGFFLKVTYVLSFTPRPDH 151
 DB 372 -----VTKNDDKRGPF----- 382
 QY 152 NDTLCHVDPS--RKGVSQRTVRLVAYAPR-DLVISRDNTPALEPOQGVNPFVLE 207
 DB 383 -CDAALDDVGETLRNQSE-----LRVYAPRLDL-----DCPSWTWPEGEPTLH 430
 QY 208 AQGQFLRLCAADSPATLSWVLQNRVLSSHPWGPRLGLEPFG-VKAGDSGRVTCR 266
 DB 431 -----CEARGNPEPS-----VHCAREDDGAVLALGLGPVTRALAGTYRCT 471
 QY 267 AENRLGSGQRALDLSVQYPPENLRVWVQANRTVLENLNGTSLPVLQSGSLCIVCTHVS 326
 DB 472 AINGQSQAVKVDLTVEYAP-----ALDSVGCPEFRTWLEGTSEASLSCVAHG 518
 QY 327 SPPARLSWTORGQVLSPESQPSDFGVLELP-RVOVEHEGEFTCHARHPGSGHVSLSLSVH 385
 DB 519 VPPPSVSCVRSGK-----EEWMEGLVAREHAGTYRCEALNAGSAAKNVATVE 569
 QY 386 YSPKL--LGPSCSW---EAGLHSCSSQAGAPSLRWLWLGSELLEGNSQDSFEVTPSS 440

Db 570 YGFSFELGCFSNWTWVEGSGKLFSCVEVDKPRVE-CVGS---EGASEGVVLPVSSN 625
 QY 441 AGPWANSSLSHGLSGLSLRCEANNVHGA 471
 Db 626 SG--SRNSMT-PGNLSEGIYL-CNATNRHGS 652
 RESULT 13
 US-08-656-984A-2
 ; Sequence 2, Application US/08656984A
 ; Patent No. 5753502
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Kilgannon, Patrick D.
 ; TITLE OF INVENTION: ICAM-4 Materials and Methods
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, C'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/08/656,984A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,689
 ; FILING DATE: 27-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/889,724
 ; FILING DATE: 26-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/894,061
 ; FILING DATE: 05-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/102,852
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/245,295
 ; FILING DATE: 18-MAY-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,604
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WILLIAMS, JR. JOSEPH A.
 ; REGISTRATION NUMBER: 38,659
 ; REFERENCE/DOCKET NUMBER: 27866/33321
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 917 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-656-984A-2

Query Match 6.8%; Score 229; DB 1; Length 917;
 Best Local Similarity 24.8%; Pred. No. 1.1e-10;
 Matches 112; Conservative 49; Mismatches 146; Indels 144; Gaps 22;

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,595
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/865,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/894,061

FILING DATE: 05-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/009,266

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/102,852

FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,295

FILING DATE: 18-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAMS, JR. JOSEPH A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32714

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 917 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-487-595-2

Query Match 6.8%; Score 229; DB 2; Length 917;

Best Local Similarity 24.8%; Pred. No. 1.1e-10; Mismatches 146; Indels 144; Gaps 22;
Matches 112; Conservative 49;

QY	32	PEGLCISVPCFSYPRQDWTGTPAYGWFKAVTETTKGAPVATNHQSRVEMSTRGRFQ	91
DB	335	PEGMVTVSC-----WAGA-----RALV-TLEGIPAAVPCQPAELQLN-----	371
QY	92	LTGDPAKGNCSLVIRDAQMDESQYFFRVERSYVRYNPMNDGPFLLKVTVLSTFTRPDH	151
DB	372	-----VTXNDKRGFP-----	382
QY	152	NTDLTCHVDFS--RKGVSAQRTVRLRVAYAPR--DLVISISRDNTFALEPQGNVPYLE	207
DB	383	-CDAALDVGDGETLRKQSS-----LRVLVAPRLDDL-----DCPRSWTWPEGEQTLH	430
QY	208	AOKGFRLLCADSQPPATLSWLVQNRVLSSHPWGPRLGLELPG-VKAGDSGRYTCR	266
DB	431	-----CEARGNPEPS-----VHCARPDGGAVALGLLGPVTRALAGTYRCT	471
QY	267	AEHLGSGQRALDLSVQYPPENLRVWVSQANRTVLENLNGTSLPVLGGQSLCLVCVTHS	326
DB	472	AINGQQAQVQVTLTVAYAP-----ALDSVCCPERITWLEGTASLSCVANG	518
QY	327	SPPARLSWTQRCQVTLSPQESDPGVLELP-RVQVEHEGEFTCHAHPLGSHQVLSLSVH	385
DB	519	VPPPSVSCVRSGK-----EENVEGPLRVAREHAGTYRCEAINARGSAAKNVATVE	569
QY	386	YSPKL--LQPSCSW---EAEGLHCSCSQASAPSLRWLGEELLEGNSSQDSFEVTPSS	440

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 74.3927 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377
Sequence: 1 MLLPLLSSLLGGSQAMDGR.....RPEARMPKGTQADYAEVKFQ 639

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3377	100.0	639	2 AAW81023	AAW81023 Human sia
2	3377	100.0	639	3 AAY97543	AAY97543 Human obe
3	3354	99.3	639	3 AAB25580	AAB25580 CD33-like
4	3354	99.3	639	6 ADA27052	ADA27052 Human nov
5	3354	99.3	639	8 ADA86582	ADA86582 Novel hum
6	3338	98.8	697	5 AAU87087	AAU87087 Sialic ac
7	3334	98.7	697	6 ADA27153	ADA27153 Human nov
8	3334	98.7	697	7 ADD26582	ADD26582 Siglec-10
9	3334	98.7	697	8 ADI37010	ADI37010 Novel hum
10	3334	98.7	697	8 ADL82805	ADL82805 Human PRO
11	3299	97.7	622	5 AAU87075	AAU87075 Sialic ac
12	3174.5	94.0	710	7 ADL19314	ADL19314 Human sec
13	2803.5	83.0	544	5 AAU87074	AAU87074 Sialic ac
14	2790.5	82.6	544	3 AAY411724	AAY411724 Human PRO
15	2790.5	82.6	544	3 AAB444280	AAB444280 Human PRO
16	2790.5	82.6	544	4 AAU29082	AAU29082 Human PRO
17	2790.5	82.6	544	6 ABU58458	ABU58458 Human PRO
18	2790.5	82.6	544	6 ABU88006	ABU88006 Novel hum
19	2790.5	82.6	544	6 ABU84321	ABU84321 Human sec
20	2790.5	82.6	544	6 ABR66195	ABR66195 Human sec
21	2790.5	82.6	544	6 ABR65585	ABR65585 Human sec
22	2790.5	82.6	544	6 ABU95925	ABU95925 Human sec
23	2790.5	82.6	544	6 ABU82764	ABU82764 Human PRO
24	2790.5	82.6	544	6 ABU89885	ABU89885 Novel hum
25	2790.5	82.6	544	6 ABR68134	ABR68134 Human sec

ALIGNMENTS

RESULT 1

AAW81023
ID AAW81023 standard; protein; 639 AA.

XX AC AAW81023;
XX XX

DT 26-APR-1999 (first entry)

DE Human sialoadhesin family 4 (SAF-1) polypeptide.

KW SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;
KW inflammation; autoimmune disease; allergy; asthma; inflammation;
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; head injury;
KW septic shock; sepsis; stroke; osteoporosis; osteoarthritis;
KW ischemia reperfusion injury; cardiovascular disease; kidney disease;
KW liver disease; myocardial infarction; hypotension; hypertension; AIDS;
KW myelodysplastic syndrome; aplastic anaemia; baldness; infection.

XX OS Homo sapiens.

XX PN WO9853840-A1.

XX PD 03-DEC-1998.

XX PF 27-MAY-1998; 98WO-US010791.

XX PR 27-MAY-1997; 97US-0047572P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Kikly KK, Erickson-Miller CL;

XX DR WPI: 1999-080779/07.

XX DR N-PSDB; RAV99911.

XX PT New sialoadhesin family 4 polypeptides and polynucleotides - useful to treat various diseases associated with SAF-4 expression.

XX PS Claim 1; Page 31; 48pp; English.

XX CC This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAV99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transfected host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

26 2790.5 82.6 544 6 ABU96187
27 2790.5 82.6 544 6 ABU92618
28 2790.5 82.6 544 6 ABO08695
29 2790.5 82.6 544 6 ABO02747
30 2790.5 82.6 544 6 ABR74901
31 2790.5 82.6 544 6 ABR94663
32 2790.5 82.6 544 6 ABO25226
33 2790.5 82.6 544 6 ABU85636
34 2790.5 82.6 544 6 ABU98796
35 2790.5 82.6 544 6 ABU98011
36 2790.5 82.6 544 6 ABU91717
37 2790.5 82.6 544 6 ABU72232
38 2790.5 82.6 544 6 ABU99410
39 2790.5 82.6 544 6 ABU86251
40 2790.5 82.6 544 6 ABU67464
41 2790.5 82.6 544 6 ABU80492
42 2790.5 82.6 544 6 ABR99410
43 2790.5 82.6 544 6 ABR98800
44 2790.5 82.6 544 6 ABO16323
45 2790.5 82.6 544 6 ABR92223

Abu96187 Novel hum
Abu92618 Human sec
Abo08695 Human sec
Abo02747 Human sec
Abr74901 Human sec
Abr94663 Human sec
Abo25226 Novel hum
Abu85636 Human PRO
Abu98796 Novel hum
Abu98011 Novel hum
Abu91717 Novel hum
Abu72232 Novel hum
Abu99410 Human PRO
Abu86251 Human sec
Abu67464 Human sec
Abu80492 Human PRO
Abr99410 Human sec
Abr98800 Human sec
Abo16323 Human sec
Abr92223 Human sec

expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypertension, hypertension, AIDS, myelodysplastic syndromes and other haematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAP-4 polypeptide activity. Methods of identifying agonists, antagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate SAP-4 activity or levels

XX Sequence 639 AA;

Query Match 100.0%; Score 3377; DB 2; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTTPAYGYW 60
 DB 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTTPAYGYW 60

QY 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFOLGTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 DB 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFOLGTGDPKAGNCSLVIRDAQMDESQYFFRV 120

QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAP 180
 DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAP 180

QY 181 RDLVISIRDNTPALPEQPGNVPYLEAQKGFRLRLCAADSQPPATLSWVLQNEVLSSS 240
 DB 181 RDLVISIRDNTPALPEQPGNVPYLEAQKGFRLRLCAADSQPPATLSWVLQNEVLSSS 240

QY 241 HPWGPRPLGLELPGVXAGDSGRVTCRAENRLGSGQALDLSVQYPENLRVWVSQANRTV 300
 DB 241 HPWGPRPLGLELPGVXAGDSGRVTCRAENRLGSGQALDLSVQYPENLRVWVSQANRTV 300

QY 301 LENLNGTSLPLVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQPSQSDPGVLELPRVQVE 360
 DB 301 LENLNGTSLPLVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQPSQSDPGVLELPRVQVE 360

QY 361 HEGEFTCHARHPLGSHVSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420
 DB 361 HEGEFTCHARHPLGSHVSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420

QY 421 GEELLEGNSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLRCEANNVHGAQSGSILQLP 480
 DB 421 GEELLEGNSQDSFEVTPSSAGFWANSSLSLHGLSSGLRLRCEANNVHGAQSGSILQLP 480

QY 481 DKKGLISTAFNSGAFIGITALLFLCLALIMKILPKRTOTETPRPRFSRHSITLDYI 540
 DB 481 DKKGLISTAFNSGAFIGITALLFLCLALIMKILPKRTOTETPRPRFSRHSITLDYI 540

QY 541 NVVPTAGPLAQKNOKATNSPRTPLPGCAPSPESKNOKKOYQLPSPEPKSSQAPES 600
 DB 541 NVVPTAGPLAQKNOKATNSPRTPLPGCAPSPESKNOKKOYQLPSPEPKSSQAPES 600

QY 601 QBSQELHLYATLNPQVRPRPRPMPKGTQADYAEVKFQ 639
 DB 601 QBSQELHLYATLNPQVRPRPRPMPKGTQADYAEVKFQ 639

RESULT 2

AA197543

ID AAY97543 standard; protein; 639 AA.

XX

XX AAY97543;

XX

DT 12-FEB-2001 (first entry)

XX Human obesity protein binding protein-2 homologue #2.
 DE Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
 XX obesity-related disorder; therapy.
 KW Homo sapiens.
 OS WO2000059942-A2.
 XX 12-OCT-2000.
 PD 22-MAR-2000; 2000WO-US006682.
 PF 02-APR-1999; 99US-0127667P.
 XX (ELIL) LILLY & CO ELI.
 PA Su EW, Wei J;
 PI WPI; 2000-664992/64.
 XX N-PSDB; AAA37848.
 DR New human obesity protein binding protein-2 homologue nucleic acids,
 PT polynucleotides and polypeptides useful for producing medicament for
 FT treating obesity and/or obesity-related disorders.
 XX Claim 9; Page 89-91; 92pp; English.
 PS This sequence is a human obesity protein binding protein-2 homologue (hOB
 CC -BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may
 CC be used for the manufacture of a medicament for the treatment of obesity
 CC and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful
 CC as probes or amplification primers in the detection, quantification or
 CC isolation of gene sequences or transcripts, for recombinant expression of
 CC hOB-BP2h polypeptides, as immunogens in the preparation and screening of
 CC antibodies, and in sense or antisense suppression of one or more hOB-BP2h
 CC genes or nucleic acids, host cell or tissue in vivo or in vitro.
 CC Antigenic epitope-bearing peptides and polypeptides are useful for
 CC raising or screening antibodies that specifically binds to the hOB-BP2h
 CC polypeptides

SQ Sequence 639 AA;

Query Match 100.0%; Score 3377; DB 3; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTTPAYGYW 60
 DB 1 MLLPILLSLLGSGQAMDGFRFIRVQESVNVPEGLCISVPCSFSPRQDWTGTTPAYGYW 60

QY 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFOLGTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 DB 61 FKAVTTTKGAPVATNHQSEVEMSTRGRFOLGTGDPKAGNCSLVIRDAQMDESQYFFRV 120

QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAP 180
 DB 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLVAYAP 180

QY 181 RDLVISIRDNTPALPEQPGNVPYLEAQKGFRLRLCAADSQPPATLSWVLQNEVLSSS 240
 DB 181 RDLVISIRDNTPALPEQPGNVPYLEAQKGFRLRLCAADSQPPATLSWVLQNEVLSSS 240

QY 241 HPWGPRPLGLELPGVXAGDSGRVTCRAENRLGSGQALDLSVQYPENLRVWVSQANRTV 300
 DB 241 HPWGPRPLGLELPGVXAGDSGRVTCRAENRLGSGQALDLSVQYPENLRVWVSQANRTV 300

QY 301 LENLNGTSLPLVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQPSQSDPGVLELPRVQVE 360
 DB 301 LENLNGTSLPLVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSQPSQSDPGVLELPRVQVE 360

QY 361 HEGEFTCHARHPLGSHVSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420
 DB 361 HEGEFTCHARHPLGSHVSLSVHYSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420

Db 361 HEGEFTCHARPLGSHQVLSLSVHYSPKLLGPGSCWEAEGHSCSSQASPAPSLRWL 420
Qy 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGGSSGLRLRCRAWNVHGAQSGSILQLP 480
Db 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGGSSGLRLRCRAWNVHGAQSGSILQLP 480
Qy 481 DKKGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRFRSHSTILDYI 540
Db 481 DKKGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRFRSHSTILDYI 540
Qy 541 NVVPTAGLAQRNKAQATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEKSTQAPES 600
Db 541 NVVPTAGLAQRNKAQATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEKSTQAPES 600
Qy 601 QESQELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 639
Db 601 QESQELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 639

RESULT 3
ID AAB25580
XX AAB25580 standard, protein; 639 AA.
AC AAB25580;
XX
DT 21-NOV-2000 (first entry)
DE CD33-like protein encoded by human secreted protein gene #5.
KW Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
KW antirheumatic; dermatological; antiproliferative; antiarteriosclerotic;
KW anticancer; vulnary; antiviral; antibacterial; antifungal;
KW immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;
KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;
KW Crohn's disease; nephritis; hyperproliferative disorder;
KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;
KW melanoma; lymphoma; wound healing; human.
XX
OS Homo sapiens.
XX
PN WO200029435-A1.
XX
XX 25-MAY-2000.
XX
PF 27-OCT-1999; 99WO-US025031.
XX
PR 28-OCT-1998; 98US-0105971P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Ruben SM, Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;
PI Greene JM;
XX
DR WPI; 2000-387742/33.
DR N-PSDB; AAA80610.
XX
PT Isolated nucleic acid molecules encoding human secreted proteins are used
PT for the prevention, amelioration and treatment of autoimmune,
PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,
PT wounds, and infectious diseases.
XX
PS Claim 1; Fig 13A-C; 803pp; English.
XX
CC The present invention relates to 12 secreted human proteins and the
CC nucleotide sequences encoding them. The polynucleotide sequences given in
CC AAB80606-A80623 encode the 12 secreted protein sequences given in
CC AAB25576-B25593. The human secreted proteins have various activities
CC dependent on the tissues in which they are expressed. Examples of the
CC activities of the proteins include: immunosuppressant; anti-inflammatory;
CC antiarthritic; antirheumatic, dermatological; antiproliferative;
CC antiarteriosclerotic; anticancer; vulnary; antiviral; antibacterial;
CC and antifungal activity. The proteins, polypeptides, agonists and

CC antagonists may be used to treat prevent and/or diagnose various disease,
CC disorders and conditions examples of which include: immune disorders e.g.
CC Addison's disease, rheumatoid arthritis, dermatitis, and multiple
CC sclerosis; inflammatory disorders e.g. inflammatory bowel disease,
CC Crohn's disease and nephritis; hyperproliferative disorders such as
CC paraproteinemias and purpura; cardiovascular disorders e.g. coronary
CC arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The
CC proteins and polynucleotide sequences may also be used in wound healing
CC and the treatment of infectious diseases. The human secreted protein gene
CC #5 and protein sequences are represented in sequences AAA80610 and
CC AAB25580. Sequences AAA80638-A80649 represent genes related to the
CC secreted protein gene#5
XX
SQ Sequence 639 AA;
Query Match 99.3%; Score 3354; DB 3; Length 639;
Best Local Similarity 99.5%; Pred. No. 1e-230;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MLLPLLLSLLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSFSPQDWTGSTPAYGW 60
Db 1 MLLPLLLSLLGGSQAMDGRFWIRVOESVMVPEGLCISVPCSFSPQDWTGSTPAYGW 60
Qy 61 FKAVTETTKGAPVATNHQREVEVMSRGRFQLTGDPKAGKNCSLVIRDAQWQDESQYFFRV 120
Db 61 FKAVTETTKGAPVATNHQREVEVMSRGRFQLTGDPKAGKNCSLVIRDAQWQDESQYFFRV 120
Qy 121 ERGSYRVNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQAQTVRLVAYAP 180
Db 121 ERGSYRVNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDVFSRKGVSQAQTVRLVAYAP 180
Qy 181 RDVVISIRDNTPALPPOQGNVPLYEAOKGQFLRLCAADSOPPATLSWVLQNRVLSSS 240
Db 181 RDVVISIRDNTPALPPOQGNVPLYEAOKGQFLRLCAADSOPPATLSWVLQNRVLSSS 240
Qy 241 HPWGPRPLGLEPLGVKAGSGRVTCAENRPLGSQLDLISVQYPPENLRVMVYSQANRTV 300
Db 241 HPWGPRPLGLEPLGVKAGSGRVTCAENRPLGSQLDLISVQYPPENLRVMVYSQANRTV 300
Qy 301 LENLNGTSLPVLGOSGLCVTHSSPPARLSWTORGVLSPSQSDPGVLELPRVOVE 360
Db 301 LENLNGTSLPVLGOSGLCVTHSSPPARLSWTORGVLSPSQSDPGVLELPRVOVE 360
Qy 361 HEGEFTCHARHPLGSHQVLSLSVHYSPKLLGPGSCWEAEGHSCSSQASPAPSLRWL 420
Db 361 HEGEFTCHARHPLGSHQVLSLSVHYSPKLLGPGSCWEAEGHSCSSQASPAPSLRWL 420
Qy 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGGSSGLRLRCRAWNVHGAQSGSILQLP 480
Db 421 GEELLEGNSQDSREVTSSAGPWANSSLSHGGSSGLRLRCRAWNVHGAQSGSILQLP 480
Qy 481 DKKGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRFRSHSTILDYI 540
Db 481 DKKGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRFRSHSTILDYI 540
Qy 541 NVVPTAGLAQRNKAQATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEKSTQAPES 600
Db 541 NVVPTAGLAQRNKAQATPNSPRTPLPGAPSPESKKNQKQYQLPSPPEKSTQAPES 600
Qy 601 QESQELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 639
Db 601 QESQELHYATLNFPGVPRPEARMKGTQADYAEVKFQ 639
RESULT 4
ADA27052
ID ADA27052 standard; protein; 639 AA.
XX
AC ADA27052;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human novel secreted protein from cDNA HDPCL05 #1.

XX cytostatic; antiinflammatory; immunomodulator; neuroprotective;
 XX hemostatic; gene therapy; cancer; inflammation; immune disorder;
 XX neurological disorder; blood clotting disorder; food additive;
 XX preservative; human; secreted protein.

XX Homo sapiens.

XX US200305231-A1.

XX 20-MAR-2003.

XX 29-OCT-2001; 2001US-00984130.

XX 28-OCT-1998; 98US-0105971P.

XX 27-OCT-1999; 99WC-US025031.

XX 19-APR-2000; 2000US-0198407P.

XX 30-OCT-2000; 2000US-0243792P.

XX 18-APR-2001; 2001US-00836353.

XX (NLIJ)/ NI J.

XX (YOUNG)/ YOUNG P E.

XX (KENN)/ KENNY J J.

XX (OLSE)/ OLSEN H S.

XX (MOOR)/ MOORE P A.

XX (WEIY)/ WEI Y.

XX (GREE)/ GREENE J M.

XX (RUBE)/ RUBEN S M.

XX (LIUD)/ LIU D.

XX (CROC)/ CROCKER P R.

XX

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NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;

Ruben SM, Liu D, Crocker PR;

WPI: 2003-567103/53.

N-PSDB; ADA27034.

New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting disorders.

Claim 11; Fig 13; 454pp; English.

The invention relates to an isolated nucleic molecule that is at least 95% identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polynucleotide fragment of the cDNA sequence contained in American Type Culture Collection (ATCC) deposit No. defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of hybridising under conditions the polynucleotide, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the secreted polypeptide (comprising a sequence that is at least 95% identical to a polypeptide fragment: domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polynucleotide or the polypeptide, the gene corresponding to the cDNA sequence and identifying an activity in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay and identifying the protein in the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide,

CC agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present is a secreted protein of the CC invention.

XX Sequence 639 AA;

Query Match 99.3%; Score 3354; DB 6; Length 639;

Best Local Similarity 99.5%; Pred. No. 1e-230;

Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFYPRQDMTGSTPAYGW 60

Db 1 MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEACDISVPCSFYPRQDMTGSTPAYGW 60

Qy 61 FKAVTETTKGAPVATNHQSHREVMSTRGPFQLTGDPKAGNCSLVIRDAQMCDSQYFVRV 120

Db 61 FKAVTETTKGAPVATNHQSHREVMSTRGPFQLTGDPKAGNCSLVIRDAQMCDSQYFVRV 120

Qy 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSQRTVLRVAYAP 180

Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDFSRKGVSQRTVLRVAYAP 180

Qy 181 RDLVISISRDNTPALBPQPGNVPLYLEAQKQFLRLCAADSOFPATLSWLNQRLVSS 240

Db 181 RDLVISISRDNTPALBPQPGNVPLYLEAQKQFLRLCAADSOFPATLSWLNQRLVSS 240

Qy 241 HPWGPRPLGLEPGVKAGDSGRVTCRAENRLGSOQALDLSVOYPPENLRVMVSOANRTV 300

Db 241 HPWGPRPLGLEPGVKAGDSGRVTCRAENRLGSOQALDLSVOYPPENLRVMVSOANRTV 300

Qy 301 LENLNGTSLPVLLEGOSLCLVCVTHSSPPARLSWTORGQVLSQSDSDPGVLELPRVQE 360

Db 301 LENLNGTSLPVLLEGOSLCLVCVTHSSPPARLSWTORGQVLSQSDSDPGVLELPRVQE 360

Qy 361 HEGEFTCHAHPLGSOHVSLSVHYSPKLLGSCSWAEAGLHCSCSSQASPAAPSLRWL 420

Db 361 HEGEFTCHAHPLGSOHVSLSVHYSPKLLGSCSWAEAGLHCSCSSQASPAAPSLRWL 420

Qy 421 GEBLEGNSSQDSFEVTPSSAGPWANSSLSHGGLSSGLRLRCEANVHGAQSGSLQLP 480

Db 421 GEBLEGNSSQDSFEVTPSSAGPWANSSLSHGGLSSGLRLRCEANVHGAQSGSLQLP 480

Qy 481 DKXGLISTAFSNGAFLEGITALLFLCLALINKILPKRTQTETPRPFSRHSITLDYI 540

Db 481 DKXGLISTAFSNGAFLEGITALLFLCLALINKILPKRTQTETPRPFSRHSITLDYI 540

Qy 541 NVVPTAGPLAOKENQKATPNSPRTPLPGAPSPESKKNOKYQLPSPFPEPKSSTQAPES 600

Db 541 NVVPTAGPLAOKENQKATPNSPRTPLPGAPSPESKKNOKYQLPSPFPEPKSSTQAPES 600

Qy 601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639

Db 601 QESQELHYATLNFPGVRPRPEARMKPGTQADYAEVKFQ 639

RESULT 5

ID ADE86582 standard; protein: 639 AA.

XX ADE86582;

XX 29-JAN-2004 (first entry)

XX Novel human secreted protein #5.

XX human; secreted protein; cancer; liver disorder; hepatitis;

KW neural disorder; Alzheimer's disease.

XX Homo sapiens.

XX US2003129685-A1.

XX


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PD 10-JUL-2003.
XX
PF 18-APR-2001; 2001US-00836353.
XX
XX 28-OCT-1998; 98US-0105971P.
PR 27-OCT-1999; 99WO-US025031.
PR 19-APR-2000; 2000US-0198407P.
XX
XX (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
XX
XX Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
PI Ruben SM;
XX
XX WPI; 2004-020335/02.
DR N-PSDB; ADB86564.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
PT preventing, treating or ameliorating a medical condition e.g. cancer,
PT liver disorders or neural disorders.
XX
XX Claim 11; SEQ ID NO 33; 380pp; English.
XX
XX The invention relates to an isolated nucleic acid sequence, or its
CC allelic variant, a fragment of the cDNA sequence, or its fragment,
CC domain, epitope or species homologue. The nucleic acid is useful for
CC preparing a medicament for preventing, treating or ameliorating a medical
CC condition e.g., cancer, liver disorders such as hepatitis or neural
CC disorders such as Alzheimer's disease. The present sequence represents
CC the amino acid sequence of a novel human secreted protein.
XX
XX Sequence 639 AA;
XX
Query Match 99.3%; Score 3354; DB 8; Length 639;
Best Local Similarity 99.5%; Pred. No. 1e-230;
Matches 636; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MLPLLLSLLGSGQAMDGRFIRYQESVWVPEGLCISVPCSFSPYPRQDWTGSTPAYGYW 60
DB 1 MLPLLLSLLGSGQAMDGRFIRYQESVWVPEACDISVPCSFSPYPRQDWTGSTPAYGYW 60
QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSVVRVNFMDGFFLKVTVLSTFPRQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
DB 121 ERGSVVRVNFMDGFFLKVTVLSTFPRQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
QY 181 RDLVISISRDNTPALEPQGNVPVLEAKQGFLLCAADSPATISWLVQNRVLSSS 240
DB 181 RDLVISISRDNTPALEPQGNVPVLEAKQGFLLCAADSPATISWLVQNRVLSSS 240
QY 241 HPWGRPRGLELPGVKAGDSGRYTCAENRLGSGQQRALDLSVQYPPENLRVWVSQANVT 300
DB 241 HPWGRPRGLELPGVKAGDSGRYTCAENRLGSGQQRALDLSVQYPPENLRVWVSQANVT 300
QY 301 LENLNGTSLPVLGGQSLCLVCVTHSSPPARLSWTQRGQVLSFSPQSPDFGVLELPRVQVE 360
DB 301 LENLNGTSLPVLGGQSLCLVCVTHSSPPARLSWTQRGQVLSFSPQSPDFGVLELPRVQVE 360
QY 361 HGEFTCHARPLGSHVLSLSVHYSPKLLGFCSSWEAGLHCSCSSQASPAPSLRWL 420
DB 361 HGEFTCHARPLGSHVLSLSVHYSPKLLGFCSSWEAGLHCSCSSQASPAPSLRWL 420
QY 421 GBELEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
DB 421 GBELEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
```

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Db 421 GBELEGNSSQDSFEVTPSSAGPWANSSLSLHGGLSSGLRCEANVHGAQSGSILQLP 480
QY 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRETQTETPRPFRSHSTILDYI 540
DB 481 DKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRETQTETPRPFRSHSTILDYI 540
QY 541 NVVPTAGPLAQNOKATNSPRTPPPGAPSPESKKNQKKQYQLSPFPSPKSTQAPES 600
DB 541 NVVPTAGPLAQNOKATNSPRTPPPGAPSPESKKNQKKQYQLSPFPSPKSTQAPES 600
QY 601 QESQELHYATLNFPGVVRPEARMKGTQADYAEVKFQ 639
DB 601 QESQELHYATLNFPGVVRPEARMKGTQADYAEVKFQ 639
XX
XX AAU87087 standard; protein; 697 AA.
XX
XX AAU87087;
XX
XX 05-JUN-2002 (first entry)
XX
XX Sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-3.
XX
XX Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
XX immune system disease; leukaemia; allergy; inflammatory disease;
XX tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
XX psoriasis; rheumatoid arthritis; conjunctivitis.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX WO200208257-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US023082.
XX
XX 21-JUL-2000; 2000US-0220139P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Longphre M, Chang H, Whitney G;
XX
XX WPI; 2002-241565/29.
XX
XX N-PSDB; ABK43373.
XX
XX Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
XX molecules useful for treating immune system diseases such as asthma,
XX leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX
XX Example 11; Fig 6; 209pp; English.
XX
XX The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
XX related lectin) protein (I). Pharmaceutical compositions comprising (I)
XX are useful for treating immune system diseases such as asthma, leukaemia
XX or other allergic or inflammatory diseases. Extracellular domains of (I)
XX represent potential markers for screening, diagnosis, prognosis, follow-
XX up assays, and imaging methods. (I) is useful as a target for drugs which
XX inhibit inflammation, tissue damage and remodeling in asthma, and
XX inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
XX disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
XX also useful for monitoring the course of disease or disorders, and for
XX identifying agents that bind with and/or modulate the biological activity
XX of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
XX useful in diagnosis and/or prognosis methods, and to detect the presence
XX and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
XX proteins in a biological sample. (II) are useful as nucleic acid probes
XX are useful for screening genomic library to isolate a genomic clone of
XX SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
XX diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
XX The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
```

CC expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
 CC AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
 CC invention
 XX
 30 Sequence 697 AA;
 1 Query Match 98.8%; Score 3338; DB 5; Length 697;
 Best Local Similarity 91.7%; Pred. No. 1.6e-229;
 Matches 639; Conservative 0; Mismatches 0; Indels 56; Gaps 1;
 1 MLLPLLSLLGSGQAMDRFWIRVQESVMVPEGLCISVPCFSYPRQDWTGSTAYGW 60
 1 MLLPLLSLLGSGQAMDRFWIRVQESVMVPEGLCISVPCFSYPRQDWTGSTAYGW 60
 61 FKAVTTTGAPVATNQHREVMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFRV 120
 61 FKAVTTTGAPVATNQHREVMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFRV 120
 121 ERGSYVRYPNMDGFFLKVT-----VLSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYARD 140
 121 ERGSYVRYPNMDGFFLKVTALTKQPDVVIPTLEPGQVTVICVENWAFESCPPPSFW 180
 141 -----VLSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYARD 182
 181 TGAALSSQGTFTTSFSLVSTPRPDHNTDLTCHVDFSRKGVSAQRTVLRVAYARD 240
 183 LVISISRDNTPALEPQGNVPYLEAQKGQFLRLCAADSQPPATLSWLQNRVLSSSH 242
 241 LVISISRDNTPALEPQGNVPYLEAQKGQFLRLCAADSQPPATLSWLQNRVLSSSH 300
 243 WGRPRPLGLELPGVKAGSGRYTCRAENRLGSGQALDLSVOYPPENLRVWVQANRTVLE 302
 301 WGRPRPLGLELPGVKAGSGRYTCRAENRLGSGQALDLSVOYPPENLRVWVQANRTVLE 360
 303 NLNGTSLPVLGQSLCLVCVTHSSPRLSWTQGVLSPPQSDPGVLELPRVQVEHE 362
 361 NLNGTSLPVLGQSLCLVCVTHSSPRLSWTQGVLSPPQSDPGVLELPRVQVEHE 420
 363 GEPTCHARPLGQHVLSLSVHSPKLLGPGSCWEAGLHSCSCSQASPAPSLRWLGE 422
 421 GEPTCHARPLGQHVLSLSVHSPKLLGPGSCWEAGLHSCSCSQASPAPSLRWLGE 480
 423 ELLEGNSDLSRFTVSSAGPWANSSLSHGLSGRLRCRANVHGAQSSILQLPDK 482
 481 ELLEGNSDLSRFTVSSAGPWANSSLSHGLSGRLRCRANVHGAQSSILQLPDK 540
 483 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTTPRFRSRHSTILDYINV 542
 541 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRTQTTPRFRSRHSTILDYINV 600
 543 VPTAGPLAKRQKATPNSPRLPLGAPSPSKNKKQYQLPFPKPSQTAPESQE 602
 601 VPTAGPLAKRQKATPNSPRLPLGAPSPSKNKKQYQLPFPKPSQTAPESQE 660
 603 SQBELHYATLNPFGVPRPEARMKPTQADYAEVFKQ 639
 661 SQBELHYATLNPFGVPRPEARMKPTQADYAEVFKQ 697

RESULT 7
 ADA27153
 ID ADA27153 standard; protein; 697 AA.
 AC
 AC ADA27153;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 DE Human novel secreted protein from cDNA HDPC05 #2.

XX cytostatic; antiinflammatory; immunomodulator; neuroprotective;
 KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KW neurological disorder; blood clotting disorder; food additive;
 KW preservative; human; secreted protein.

XX Homo sapiens.
 OS US2003055231-A1.
 PN 20-MAR-2003.
 PD 29-OCT-2001; 2001US-00984130.
 PF 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.
 XX (NLIJ/) NI J.
 PA (YOUN/) YOUNG P E.
 PA (KEND/) KENNY J J.
 PA (OLSE/) OLSEN H S.
 PA (MOOR/) MOORE P A.
 PA (WEIY/) WEI Y.
 PA (GREE/) GREENE J M.
 PA (RUBE/) RUBEN S M.
 PA (LIUD/) LIU D.
 PA (CROC/) CROCKER P R.
 XX NI J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 FI Ruben SM, Liu D, Crocker PR;
 PI MPI: 2003-567103/53.
 DR N-PSDB; ADA27152.
 XX
 PT New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 PS Claim 11; Page 383-385; 454pp; English.
 XX
 CC The invention relates to an isolated nucleic molecule that is at least
 CC 95% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC defined in the specification, its species homologue, a variant or allelic
 CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridising under conditions the polynucleotide, where the polynucleotide
 CC does not hybridise under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide), the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity
 CC in a biological assay and identifying the protein in the supernatant
 CC having the activity). The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, such as cancer, inflammation and other immune
 CC disorders, neurological and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present is a secreted protein of the
 CC invention.

```
SQ      Sequence 697 AA;
Query Match      98.7%; Score 3334; DB 6; Length 697;
Best Local Similarity 91.5%; Pred. No. 3e-229;
Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY      1 MLPLLLSSLLGGSQAMDGFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
DQ      1 MLPLLLSSLLGGSQAMDGFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
QY      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
DQ      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
QY      121 ERGSYRYNFMNDGFLKVT----- 140
DQ      121 ERGSYRYNFMNDGFLKVT----- 140
QY      141 -----VLSLTPRPDQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 182
DQ      181 TGAALSSQGTPTTSHFSVLTSTPRPDQDHTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
QY      183 LVISIRSDNTPALEPOQGNVPEYLAQKQFLLELCAADSQPPATLSWYLNQNRVLSSSH 242
DQ      241 LVISIRSDNTPALEPOQGNVPEYLAQKQFLLELCAADSQPPATLSWYLNQNRVLSSSH 300
QY      243 WGPRLPLGLELPGVKGADSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSOANETVLE 302
DQ      301 WGPRLPLGLELPGVKGADSGRYTCRAENRLGSOQRALDLSVOYPPENLRVMVSOANETVLE 360
QY      303 NLGNQTSLEVLGQSCLVCTVTHSSPPARLSWTQGVLSQPSQDPGVLELPRVQVEHE 362
DQ      361 NLGNQTSLEVLGQSCLVCTVTHSSPPARLSWTQGVLSQPSQDPGVLELPRVQVEHE 420
QY      363 GEFTCHARPLGSHVLSLSVHYGPKLGLGSCSWEAELHSCSSQASPPASLRLWLGE 422
DQ      421 GEFTCHARPLGSHVLSLSVHYGPKLGLGSCSWEAELHSCSSQASPPASLRLWLGE 480
QY      423 ELLEGNSQDSPEVTPSSAGPWANGLSLHGLSSGLRLRCBANNVHGAQSGSILQLPDK 482
DQ      481 ELLEGNSQDSPEVTPSSAGPWANGLSLHGLSSGLRLRCBANNVHGAQSGSILQLPDK 540
QY      483 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRPSRHSITLDYINV 542
DQ      541 KGLISTAFNGAFLGIGITALLFLCLALIMKILPKRRTQTTPRPSRHSITLDYINV 600
QY      543 VTAGPLAQRNKAQATENSPTPLPPGAPSPESKKNQKQYOLPSPFPKSTQAPESQE 602
DQ      601 VTAGPLAQRNKAQATENSPTPLPPGAPSPESKKNQKQYOLPSPFPKSTQAPESQE 660
QY      603 SOEELHYATLNFPGVRRPEARMKPGTQADYAEVKFQ 639
DQ      661 SOEELHYATLNFPGVRRPEARMKPGTQADYAEVKFQ 697

RESULT 8
ADD26582
ID      ADD26582 standard; protein; 697 AA.
XX
AC      ADD26582;
XX
DT      15-JAN-2004 (first entry)
XX
DE      Siglec-10 amino acid sequence SEQ ID NO:7.
XX
KW      human; cell surface protein; immunoglobulin; BGS-19; cytostatic;
KW      gynaecological; immunosuppressive; antiinflammatory; antiasthmatic;
KW      antidiabetic; dermatological; gene therapy.
XX
OS      Homo sapiens.
XX
PN      WC02003083078-A2.
XX
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PD      09-OCT-2003.
XX
PF      28-MAR-2003; 2003WO-US009676.
XX
PR      28-MAR-2002; 2002US-0368422P.
XX
PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI      Lee LM, Feder JN, Siemers NQ, Wu S, Chen J;
XX
WPI; 2003-804052/75.
XX
New isolated nucleic acid molecule encoding BGS-19 polypeptides, useful
for preventing, treating or ameliorating a medical condition, such as a
PT disorder related to aberrant immunoglobulin cell surface receptor
PT activity.
XX
Example 1; SEQ ID NO 7; 224pp; English.
XX
The present invention describes human cell surface protein with
immunoglobulin folds, designated BGS-19 (I). (i) has cytosolic,
gynaecological, immunosuppressive, antiinflammatory, antiasthmatic,
antidiabetic and dermatological activities, and can be used in gene
therapy. (ii) can be used for preventing, treating or ameliorating a
medical condition, such as a disorder related to aberrant immunoglobulin
cell surface receptor activity; a cellular adhesion disorder; a disorder
related to hyper- or hypo-immunoglobulin receptor activity; a disorder
related to aberrant signal transduction; a reproductive disorder; a
female reproductive disorder; an ovarian disorder; ovarian cancer; a
dysfunctional uterine bleeding; amenorrhoea; primary dysmenorrhoea;
sexual dysfunction; infertility; pelvic inflammatory disease;
endometriosis; placental aromatase deficiency; premature menopause;
placental dysfunction; hormone deficiency; oestrogen deficiency; aberrant
androgen metabolism; aberrant onset of female puberty; aberrant showing
of female primary sexual characteristics; aberrant showing of female
secondary sexual characteristics; precocious puberty; precocious
pseudopuberty; incomplete isosexual precocity; premature thelarche;
premature adrenarche; premature pubarche; polycystic ovarian disease;
aberrant ovarian cycle; menorrhagia; metrorrhagia; menometrorrhagia;
dysmenorrhoea; hypomenorrhoea; polymenorrhoea; dysfunctional uterine
bleeding; resistant-ovary syndrome; hermaphroditism; immune disorders;
inflammatory disorders; arthritis; asthma; immunodeficiency diseases such
as AIDS; leukaemia; rheumatoid arthritis; granulomatous disease;
inflammatory bowel disease; sepsis; acne; neutropenia; neutrophilia;
psoriasis; hypersensitivities; such as T-cell mediated cytotoxicity;
immune reactions to transplanted organs and tissues; such as host-versus-
graft and graft-versus-host diseases; or autoimmune disorders;
autoimmune infertility; Addison's disease; haemolytic anaemia;
antiphospholipid syndrome; rheumatoid arthritis; dermatitis; allergic
encephalomyelitis; glomerulonephritis; Goodpasture's Syndrome; Graves'
Disease; Multiple Sclerosis; Myasthenia Gravis; Neuritis; Ophthalmia;
Bullous Pemphigoid; Pemphigus; Polyendocrinopathies; Purpura; Reiter's
Disease; Stiff-Man Syndrome; autoimmune thyroiditis; Systemic Lupus
Erythematosus; Autoimmune Pulmonary Inflammation; Guillain-Barre Syndrome
; insulin dependent diabetes mellitus; autoimmune inflammatory eye
disease; lens tissue injury; demyelination; systemic lupus erythematosus;
drug induced haemolytic anaemia; rheumatoid arthritis; Sjogren's disease;
and scleroderma. The present sequence is given in comparison with BGS-19
in the present invention.
XX
SQ      Sequence 697 AA;
```

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Query Match      98.7%; Score 3334; DB 7; Length 697;
Best Local Similarity 91.5%; Pred. No. 3e-229;
Matches 638; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY      1 MLPLLLSSLLGGSQAMDGFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
DQ      1 MLPLLLSSLLGGSQAMDGFWIRVOESVMVPEGLCISVPCSFSPRODWTGSTPAYGYW 60
QY      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
DQ      61 FKAVTETTKGAPVATNHQSRVEMSTRGRFQLTGDPKAGNCSLVIRDAQWQDSQYFFRV 120
```

121 ERGSYVRYNFMNDGFLKVT----- 140
 121 ERGSYVRYNFMNDGFLKVTALTKPDVYIPETLBPQPVTVICVFNWAFECPPPSFW 180
 141 -----VLSFTPRQDHTDCHVDFSRKGVSAQRTVRLVAVAPRD 182
 181 TGAALSSQGTTPPTSHFVSLSFTPRQDHTDCHVDFSRKGVSAQRTVRLVAVAPRD 240
 183 LVISISRDNTPALEPQPGNVVYLEAQGFRLLCADSPATLSWLVQNRVLSSSH 242
 241 LVISISRDNTPALEPQPGNVVYLEAQGFRLLCADSPATLSWLVQNRVLSSSH 300
 243 WGRPRPLGLELPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 302
 301 WGRPRPLGLELPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 360
 303 NLGNGTSLPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 362
 361 NLGNGTSLPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 420
 363 GEFTCHARHPLGSHVLSLSVHYSPKLGPSCSWEAGLHCSCSSQASPA 422
 421 GEFTCHARHPLGSHVLSLSVHYSPKLGPSCSWEAGLHCSCSSQASPA 480
 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCCEANVHGAQSG 482
 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCCEANVHGAQSG 540
 483 KGLISTAFNSGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRSHST 542
 541 KGLISTAFNSGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRSHST 600
 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKXKQKQYQLPSPPEKSTQ 602
 601 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKXKQKQYQLPSPPEKSTQ 660
 603 SOBELHYATLNFPGVPRPEARMPKGTQADYAEVKFQ 639
 661 SOBELHYATLNFPGVPRPEARMPKGTQADYAEVKFQ 697

RESULT 9

AD137010
 ID AD137010 standard; protein; 697 AA.

XX AC AD137010;

XX DT 22-APR-2004 (first entry);

XX DE Novel human secreted and transmembrane protein PRO 71236.

XX KW human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic factor; hormone; cell receptor;
 KW receptor-ligand interaction; cytoskeletal; chondrocyte; tumour.

XX CS Homo sapiens.

XX PN WO2004004649-A2.

XX PD 15-JAN-2004.

XX PF 08-JUL-2003; 2003WO-US021083.

XX PR 08-JUL-2002; 2002US-0394485P.

XX PA (GETH) GENENTECH INC.

XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld J, Wood W, Wu T;

XX DR WPI; 2004-142912/14.

DR N-PSDB; AD137009.

PS Claim 10; SEQ ID NO 10; 118pp; English.

CC This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neurotrophic factors and hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytostatic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.

XX Sequence 697 AA;

Query Match 98.7%; Score 3334; DB 8; Length 697;

Best Local Similarity 91.5%; Pred. No. 3e-229;

Matches 538; Conservative 0; Mismatches 1; Indels 58; Gaps 1;

QY 1 MLLPLLSSLLGSSQADGDFWIRVQESVNVVPGCLISVPCSSYPRQMTGTTPAYGW 60

DB 1 MLLPLLSSLLGSSQADGDFWIRVQESVNVVPGCLISVPCSSYPRQMTGTTPAYGW 60

QY 61 FKAVTETTKGAPVATNHQSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDSSQYFFRV 120

DB 61 FKAVTETTKGAPVATNHQSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDSSQYFFRV 120

QY 121 ERGSYVRYNFMNDGFLKVT----- 140

DB 121 ERGSYVRYNFMNDGFLKVTALTKPDVYIPETLBPQPVTVICVFNWAFECPPPSFW 180

QY 141 -----VLSFTPRQDHTDCHVDFSRKGVSAQRTVRLVAVAPRD 182

DB 181 TGAALSSQGTTPPTSHFVSLSFTPRQDHTDCHVDFSRKGVSAQRTVRLVAVAPRD 240

QY 183 LVISISRDNTPALEPQPGNVVYLEAQGFRLLCADSPATLSWLVQNRVLSSSH 242

DB 241 LVISISRDNTPALEPQPGNVVYLEAQGFRLLCADSPATLSWLVQNRVLSSSH 300

QY 243 WGRPRPLGLELPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 302

DB 301 WGRPRPLGLELPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 360

QY 303 NLGNGTSLPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 362

DB 361 NLGNGTSLPVLEQSGSLVSVHYSPKLGPSCSWEAGLHCSCSSQASPA 420

QY 363 GEFTCHARHPLGSHVLSLSVHYSPKLGPSCSWEAGLHCSCSSQASPA 422

DB 421 GEFTCHARHPLGSHVLSLSVHYSPKLGPSCSWEAGLHCSCSSQASPA 480

QY 423 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCCEANVHGAQSG 482

DB 481 ELLEGNSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLRCCEANVHGAQSG 540

QY 483 KGLISTAFNSGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRSHST 542

DB 541 KGLISTAFNSGAFLGIGITALLFLCLALIMKILPKRRTQTETPRFRSHST 600

QY 543 VPTAGPLAQRNOKATPNSPRTPLPGAPSPESKXKQKQYQLPSPPEKSTQ 602

Db 601 VTAGPLAQRNKAQTPNSPRPLPGAPSPESKKNQKQYQLPSFPFKSSTQAPESQ 660
 QY 603 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 639
 Db 661 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 10
 ADL82805
 ID ADL82805 standard; protein; 697 AA.
 AC ADL82805;
 DT 17-JUN-2004 (first entry)
 DE Human PRO71236, SEQ ID 7.
 KW Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;
 KW Gene Therapy; PRO; B cell related disorder; Cancer;
 KW immune-mediated inflammatory disease; human.
 OS Homo sapiens.
 XX WO2004024097-A2.
 XX 25-MAR-2004.
 XX 15-SEP-2003; 2003WO-US029097.
 XX 16-SEP-2002; 2002US-0411392P.
 PR (GETH) GENENTECH INC.
 PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
 PI Wu TD;
 FI WPI; 2004-329389/30.
 DR N-PSDB; ADL82804.
 XX New PRO polypeptide, useful for diagnosing and treating a B cell related
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
 XX Claim 10; Fig 7; 695pp; English.

CC The present invention relates to PRO proteins and their coding sequences.
 CC The PRO proteins are useful for diagnosing and treating a B cell related
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
 CC antigen unresponsiveness, selective IgA deficiency, selective IgM
 CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
 CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
 CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 CC coding sequences are useful as hybridization probes in chromosome and
 CC gene mapping, in preparing PRO proteins, or in generating transgenic
 CC animals or knockout animals, which in turn are useful in the development
 CC and screening of therapeutically useful reagents.

XX Sequence 697 AA;
 Query Match 98.7%; Score 3334; DB 8; Length 697;
 Best Local Similarity 91.5%; Pred No 3e-229; Indels 58; Gaps 1;
 Matches 638; Conservative 0; Mismatches 1;

QY 1 MLLPILLSLLGSGQAMDRFIRVQESVMVPEGLCISVPCSFYSPRODWTGSTPAYCYW 60
 Db 1 MLLPILLSLLGSGQAMDRFIRVQESVMVPEGLCISVPCSFYSPRODWTGSTPAYCYW 60

QY 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMDSSQYFFRV 120
 Db 61 FKAVTETTKGAPVATNHQSRREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMDSSQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVT----- 140
 Db 121 ERGSYVRYNFMNDGFFLKVTALTKQPDVYIPETLEPGQPVTVICVFNWAECEPPPSFSW 180
 QY 141 -----VLSFTPRPDHNTDUTCHVDFSRKGVSAQRTVLRVAVAPRD 182
 Db 181 TGAALSSQGTKPTTSHFSLVSTFTPRPDHNTDUTCHVDFSRKGVSVQRTVLRVAVAPRD 240
 QY 183 LVTSISRDNTPALEPQGNVPYLEAKQGFLLCAADSOPTATLSWLQNRVLSSSH 242
 Db 241 LVTSISRDNTPALEPQGNVPYLEAKQGFLLCAADSOPTATLSWLQNRVLSSSH 300
 QY 243 WGRPLGLELPFGKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSAQNRVLE 302
 Db 301 WGRPLGLELPFGKAGDSGRYTCRAENRLGSOQRALDLSVQYPPENLRVMVSAQNRVLE 360
 QY 303 NLNGTSLPVLEQSLCLVCVTHSSPPARLSWTQRGQVLSQSPSDPGVLELPRVQVEHE 362
 Db 361 NLNGTSLPVLEQSLCLVCVTHSSPPARLSWTQRGQVLSQSPSDPGVLELPRVQVEHE 420
 QY 363 GEFTCHARHPLGSOHVSLSLSVHYSPKLLGPSCSWEAEGHLCSCSSOASPAISLRWMLGE 422
 Db 421 GEFTCHARHPLGSOHVSLSLSVHYSPKLLGPSCSWEAEGHLCSCSSOASPAISLRWMLGE 480
 QY 423 ELLEGNSSQDSFEVTPSSAGFWANSSLSLHGGSSGLRLRCEANVHGAQSGSILQLPDK 482
 Db 481 ELLEGNSSQDSFEVTPSSAGFWANSSLSLHGGSSGLRLRCEANVHGAQSGSILQLPDK 540
 QY 483 KGLISTAFSNGAFILGIGITALFLCLALIMKILPKRRTOTETPRFRFSRHSHTILDYINV 542
 Db 541 KGLISTAFSNGAFILGIGITALFLCLALIMKILPKRRTOTETPRFRFSRHSHTILDYINV 600
 QY 543 VPTAGPLAQRNKAQTPNSPRPLPGAPSPESKKNQKQYQLPSFPFKSSTQAPESQ 602
 Db 601 VPTAGPLAQRNKAQTPNSPRPLPGAPSPESKKNQKQYQLPSFPFKSSTQAPESQ 660
 QY 603 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 639
 Db 661 SOBELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 697

RESULT 11
 AAU87075
 ID AAU87075 standard; protein; 622 AA.
 AC AAU87075;
 DT 05-JUN-2002 (first entry)
 DE Sialic acid-binding Ig-related lectin, Siglec-BMS-L3b.
 KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
 KW immune system disease; leukaemia; allergy; inflammatory disease;
 KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
 KW psoriasis; rheumatoid arthritis; conjunctivitis.
 OS Homo sapiens.
 XX WO200208257-A2.
 XX 31-JAN-2002.
 XX 20-JUL-2001; 2001WO-US023082.
 XX 21-JUL-2000; 2000US-0220139P.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.

pi Longphre M, Chang H, Whitney G;
xx WPI; 2002-241565/29.
xx N-PSDB; ABK43361.
Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
molecules useful for treating immune system diseases such as asthma,
leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
Claim 5; Fig 3B; 209pp; English.
The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
related lectin) protein (I). Pharmaceutical compositions comprising (I)
are useful for treating immune system diseases such as asthma, leukaemia
or other allergic or inflammatory diseases. Extracellular domains of (I)
represent potential markers for screening, diagnosis, prognosis, follow-
up assays, and imaging methods. (I) is useful as a target for drugs which
inhibit inflammation, tissue damage and remodeling in asthma, and
inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
also useful for monitoring the course of disease or disorders, and for
identifying agents that bind with and/or modulate the biological activity
of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
useful in diagnosis and/or prognosis methods, and to detect the presence
and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
proteins in a biological sample. (II) are useful as nucleic acid probes
are useful for screening genomic library to isolate a genomic clone of
SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
invention
xx
xx
xx Sequence 622 AA;
Query Match 97.7%; Score 3299; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 8.1e-227;
Matches 622; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
18 DGRFWIRVQESVWVPGGLCISVPCSFYPRQDWTGTPAYGVFRAVETTTKGAPVAINH 77
1 DGRFWIRVQESVWVPGGLCISVPCSFYPRQDWTGTPAYGVFRAVETTTKGAPVAINH 60
78 QSRVEMSTRGRQLTGDFPAKNCISVIRDAQMDQESQYFFRVERGSYVRYNFMNDGFLL 137
61 QSRVEMSTRGRQLTGDFPAKNCISVIRDAQMDQESQYFFRVERGSYVRYNFMNDGFLL 120
138 KTVLSFTPRPDHNTDLTCHVDPSKGYSAQRTVRLRVAYAPRDLVISISRDNTPALEP 197
121 KTVLSFTPRPDHNTDLTCHVDPSKGYSAQRTVRLRVAYAPRDLVISISRDNTPALEP 180
198 QPGQNPVYLEAQKQFLRLLCADSPATLSVNLQNRVLSSSHHPGPRPLGLELPGVKA 257
181 QPGQNPVYLEAQKQFLRLLCADSPATLSVNLQNRVLSSSHHPGPRPLGLELPGVKA 240
258 GDSGRVTCRAENRGLSQDALDLSVQYPENLRVMSQANRVLENLNGTSLPVLGQS 317
241 GDSGRVTCRAENRGLSQDALDLSVQYPENLRVMSQANRVLENLNGTSLPVLGQS 300
318 LCUCVTHSSPPARLSWTORGQVLSQSDPQVLELPRVQVEHEGEFTCHARHPLGSGH 377
301 LCUCVTHSSPPARLSWTORGQVLSQSDPQVLELPRVQVEHEGEFTCHARHPLGSGH 360
378 VLSLSVHVSPLLGPSCWAEGLHCSCSSQASAPSLRWLGGELLEGNSQSFEVT 437
361 VLSLSVHVSPLLGPSCWAEGLHCSCSSQASAPSLRWLGGELLEGNSQSFEVT 420
438 PSSAGPWANSSLSHGLSSGLRLRCRAENVHGAQSGSILQPKKGLISTAFSNGAFLG 497
421 PSSAGPWANSSLSHGLSSGLRLRCRAENVHGAQSGSILQPKKGLISTAFSNGAFLG 480
498 IGTALLFLCLALIIWKILPKRTQTETPRPRSRHSTILDYINVVPTAGLAQRNOKA 557

Db 481 IGTALLFLCLALIIWKILPKRTQTETPRPRSRHSTILDYINVVPTAGLAQRNOKA 540
Qy 558 TPNSPRTPLPAGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQESQELHYATLNPVG 617
Db 541 TPNSPRTPLPAGAPSPSKKNQKQYQLPSPFPKSKSTQAPESQESQELHYATLNPVG 600
Qy 618 RRPPEARMPKGTQADYAEVKFQ 639
Db 501 RRPPEARMPKGTQADYAEVKFQ 622
RESULT 12
ADD19314
ID ADD19314 standard; protein; 710 AA.
XX ADD19314;
AC ADD19314;
XX
DT 15-JAN-2004 (first entry)
XX Human secreted protein from gene 18 #3.
XX human secreted protein; cytostatic; antibacterial; virucide;
KW neuroprotective; gynaecological; gastrointestinal-Gen; cardiac;
KW cardiovascular-Gen; nephrotropic; anti-inflammatory; muscular-Gen;
KW respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic;
KW neotropic; anti-allergic; cancer; bacterial infection; viral infection;
KW neural disorder; immune system disorder; blood disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW inflammatory disorder; proliferative disorder; human.
XX
OS Homo sapiens.
XX
XX WO2003052377-A2.
XX
PD 26-JUN-2003.
XX
XX 06-NOV-2002; 2002WO-US035606.
XX
XX 07-NOV-2001; 2001US-0331046P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI; 2003-533050/50.
XX N-PSDB; ADD19239.
XX
XX New isolated nucleic acids encoding signal transduction pathway component
polypeptides, useful for diagnosing, treating, and/or preventing
disorders, such as cancer, infections, cardiovascular and inflammatory
diseases.
XX
XX Claim 11; SEQ ID NO 141; 554pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (cDNA)
encoding a human secreted protein, representing one of 85 novel genes.
XX Also included are recombinant vectors, host cells (expressing the
protein), the secreted proteins (including their fragments, epitopes and
homologues), an isolated antibody that binds specifically to the protein,
XX diagnosing a pathological condition or susceptibility to a pathological
condition (comprising determining the presence or absence of a mutation
in the nucleic acid and diagnosing a condition based on the presence or
XX absence of the mutation), diagnosing a pathological condition or
susceptibility to a pathological condition (comprising determining the
XX presence or amount of expression of the protein in a biological sample
and diagnosing a condition based on the presence or amount of expression
XX of the protein), preventing, treating or ameliorating a medical condition
XX by administering the nucleic acid or protein to a mammalian subject,
XX identifying a binding partner to the protein, the gene corresponding to
the cDNA sequence, and identifying an activity in a biological assay
XX (comprising expressing the nucleic acid in a cell, isolating the

CC supernatant, detecting an activity in a biological assay and identifying
CC the protein in the supernatant having the activity). The nucleic acids
CC and proteins display the following activities: Cytostatic, antibacterial,
CC virucide, Neuroprotective, Gynaecological, Gastrointestinal-Gen,
CC Cardiac, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-
CC Respiratory-Gen, Immunosuppressive, Cerebroprotective, Vasotropic,
CC Nootropic, Antiallergic. The methods and compositions of the present
CC invention are useful for diagnosing, treating, preventing and/or
CC prognosticating disorders related to the novel polypeptides, such as
CC cancer, bacterial or viral infections, and neural, immune system, blood,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, inflammatory or proliferative disorders (many examples of these
CC diseases and disorders are given in the specification). The present
CC sequence represents a novel secreted protein of the invention.
XX
SQ Sequence 710 AA;

Query Match 94.0%; Score 3174.5; DB 7; Length 710;
Best Local Similarity 89.4%; Pred. No. 7.6e-218; Indels 61; Gaps 2;
Matches 610; Conservative 2; Mismatches 9;
QY 19 GRFWIRVQESVMVPE---GLCISVPCSFSPYRQDWGTGTPAYGWFKAIVTTTKGAPVAT 75
DB 29 GYGWILDTSGVSDGAGGLCISVPCSFSPYRQDWGTGTPAYGWFKAIVTTTKGAPVAT 88
QY 76 NQOSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRVERGSYRYNFMNDGF 135
DB 89 NQOSREVMSTGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRVERGSYRYNFMNDGF 148
QY 136 FLKVT----- 140
DB 149 FLKVTALTKQPDVYIPETLEPGQPVTVICVFNWAFEECPSPFSWGTGAALSQGTPTTS 208
QY 141 ---VLSTFRPDQDHTDITCHVDFSRKGVSAQRTVRLRVAVAPRDLVTSISRDNTPALEP 197
DB 209 HFSVLSFTFRPDQDHTDITCHVDFSRKGVSAQRTVRLRVAVAPRDLVTSISRDNTPALEP 268
QY 198 OPGNVVLEAKQGFLLCAADSOBPAATLSWLQNEVLSSSHWPGRPLGLELPGVKA 257
DB 269 OPGNVVLEAKQGFLLCAADSOBPAATLSWLQNEVLSSSHWPGRPLGLELPGVKA 328
QY 258 GDSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVMSQANRTVLENLGNSTSLPVEGQS 317
DB 329 GDSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVMSQANRTVLENLGNSTSLPVEGQS 388
QY 318 LCLVCTHSSPPARLSWTORGVLSPSPQSPDPGVLELPRVQVEHEGFTCHARHPLGSOH 377
DB 389 LCLVCTHSSPPARLSWTORGVLSPSPQSPDPGVLELPRVQVEHEGFTCHARHPLGSOH 448
QY 378 VSLSLSVHYSPKLLGFCSCWEAGLHCSCSQASPAFLRWLWLBELLEGNSQDSFEVT 437
DB 449 VSLSLSVHYSPKLLGFCSCWEAGLHCSCSQASPAFLRWLWLBELLEGNSQDSFEVT 508
QY 438 PSSAGFWANSSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFNGAPLG 497
DB 509 PSSAGFWANSSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLPDKKGLISTAFNGAPLG 568
QY 498 IGITALLFLCALITMKILPKERTOTETPRFRFSHSTILDYINVVPTAGPLAKRNOKA 557
DB 569 IGITALLFLCALITMKILPKERTOTETPRFRFSHSTILDYINVVPTAGPLAKRNOKA 628
QY 558 TNSPRTPLPPGAPSPESKQKQYQLPSPFPKSSSTQAPESQSBELHYATLNFPGV 617
DB 629 TNSPRTPLPPGAPSPESKQKQYQLPSPFPKSSSTQAPESQSBELHYATLNFPGV 686
QY 618 RRPPEARPKGTQADYAEVKFQ 639
DB 669 RRPPEARPKGTQADYAEVKFQ 710

RESULT 13
AAU87074
ID AAU87074 standard; protein; 544 AA.

XX AAU87074;
XX
XX 05-JUN-2002 (first entry)
XX
XX Sialic acid-binding Ig-related lectin, Siglec-BMS-13a.
DE
XX Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
XX immune system disease; leukaemia; allergy; inflammatory disease;
KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
KW psoriasis; rheumatoid arthritis; conjunctivitis.
XX
OS Homo sapiens.
XX
XX WO200208257-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US023082.
XX
XX 21-JUL-2000; 2000US-0220139P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Longphre M, Chang H, Whitney G;
XX
XX WPI; 2002-241565/29.
DR
XX N-PSDB; ABK43360.
XX
XX Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein
PT molecules useful for treating immune system diseases such as asthma,
PT leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.
XX
XX Claim 5; Fig 2B; 209pp; English.
XX
XX The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
CC related lectin) protein (I). Pharmaceutical compositions comprising (I)
CC are useful for treating immune system diseases such as asthma, leukaemia
CC or other allergic or inflammatory diseases. Extracellular domains of (I)
CC represent potential markers for screening, diagnosis, prognosis, follow
CC up assays, and imaging methods. (I) is useful as a target for drugs which
CC inhibit inflammation, tissue damage and remodeling in asthma, and
CC inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's
CC disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is
CC also useful for monitoring the course of disease or disorders, and for
CC identifying agents that bind with and/or modulate the biological activity
CC of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are
CC useful in diagnosis and/or prognosis methods, and to detect the presence
CC and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS
CC proteins in a biological sample. (II) are useful as nucleic acid probes
CC are useful for screening genomic library to isolate a genomic clone of
CC SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting
CC diseases or disorders associated with SIGLEC-BMS transcripts or proteins.
CC The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells
CC expressing SIGLEC-BMS proteins and in diagnostic imaging technology.
CC AAU87074-AAU87089 represent human SIGLEC amino acid sequences of the
CC invention
XX
XX Sequence 544 AA;

Query Match 83.0%; Score 2803.5; DB 5; Length 544;
Best Local Similarity 85.1%; Pred. No. 1.7e-191;
Matches 544; Conservative 0; Mismatches 0; Indels 95; Gaps 1;
QY 1 MLLPLLSLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYRQDWGTGTPAYGW 60
DB 1 MLLPLLSLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYRQDWGTGTPAYGW 60
QY 61 FKAVTETTKGAPVATNHQSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATNHQSEVEMSTGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
QY 121 ERGSYRYNFMNDGFFLKVTVLSFTFRPDQDHTDITCHVDFSRKGVSAQRTVRLRVAYAP 180

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121 ERGSYRVNFMNDGFFLKVTLVSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
181 RLIVISISDNTPALBPQGNVPYLEAQKGQFLRLCAADSPQATLSWLQNRVLSSS 240
181 RLIVISISDNTPALBPQGNVPYLEAQKGQFLRLCAADSPQATLSWLQNRVLSSS 240
241 HPWGPRLGLELPGVKAGSPGRYTCRAENRLGSOQRALDLSVQYPPENLRVWVSQANRTV 300
241 HPWGPRLGLELPGVKAGSPGRYTCRAENRLGSOQRALDLSVQYPPENLRVWVSQANRTV 300
301 LENLGNCTSLPVLGOSLCLVCVTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVE 360
301 LENLGNCTSLPVLGOSLCLVCVTHSSPPARLSWTORGQVLSPPSPGVLLEPRVQVE 360
361 HEGEFTCHARHPLGSOHVSLSVHSPKXJLGPSCWEAEGLHCSQASQAPSLRWL 420
361 HEGEFTCHARHPLGSOHVSLSVHSPKXJLGPSCWEAEGLHCSQASQAPSLRWL 420
421 GEELEGNSSQDSFEVTPSSAGPWANSSLSLHGLSSGLRLCEANVHGAQSGSILQLP 480
387 ----- 386
481 DKKGLISTAFSNGAFIGITALLFLCLALIMKILPKRTOTETPRFRSHSTILDYI 540
387 -KKGLISTAFSNGAFIGITALLFLCLALIMKILPKRTOTETPRFRSHSTILDYI 445
541 NVVPTAGPLAQKRNOKATPNSPRTPLPGAPSPESKKNQKQYOLPSPPEKKSSTQAPES 600
446 NVVPTAGPLAQKRNOKATPNSPRTPLPGAPSPESKKNQKQYOLPSPPEKKSSTQAPES 505
601 QBSQELHYATLNEPCVRPEARMKPGTQADYAEVKQ 639
506 QBSQELHYATLNEPCVRPEARMKPGTQADYAEVKQ 544

RESULT 14
AAV41724
ID AAY41724 standard; protein; 544 AA.
XX AC AAY41724;
XX AC AAY41724;
XX DT 07-DEC-1999 (first entry)
XX DE Human PRO940 protein sequence.
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
XX KW secreted protein; transmembrane protein.
XX OS Homo sapiens.
XX PN WO9946281-A2.
XX PD 16-SEP-1999.
XX XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1998; 98US-0077450P.
XX 11-MAR-1998; 98US-0077632P.
XX 11-MAR-1998; 98US-0077641P.
XX 11-MAR-1998; 98US-0077649P.
XX 12-MAR-1998; 98US-0077791P.
XX 13-MAR-1998; 98US-0078004P.
XX 17-MAR-1998; 98US-0040220.
XX 20-MAR-1998; 98US-0078886P.
XX 20-MAR-1998; 98US-0078910P.
XX 20-MAR-1998; 98US-0078938P.
XX 20-MAR-1998; 98US-0078939P.
XX 25-MAR-1998; 98US-0079294P.
XX 26-MAR-1998; 98US-0079656P.
XX 27-MAR-1998; 98US-0079663P.
XX 27-MAR-1998; 98US-0079664P.
27-MAR-1998; 98US-0079689P.
27-MAR-1998; 98US-0079728P.
27-MAR-1998; 98US-0079786P.
30-MAR-1998; 98US-0079920P.
30-MAR-1998; 98US-0079923P.
31-MAR-1998; 98US-0080105P.
31-MAR-1998; 98US-0080107P.
31-MAR-1998; 98US-0080165P.
31-MAR-1998; 98US-0080194P.
01-APR-1998; 98US-0080327P.
01-APR-1998; 98US-0080328P.
01-APR-1998; 98US-0080333P.
01-APR-1998; 98US-0080334P.
08-APR-1998; 98US-0081049P.
08-APR-1998; 98US-0081070P.
08-APR-1998; 98US-0081071P.
09-APR-1998; 98US-0081195P.
09-APR-1998; 98US-0081203P.
09-APR-1998; 98US-0081229P.
15-APR-1998; 98US-0081817P.
15-APR-1998; 98US-0081838P.
15-APR-1998; 98US-0081952P.
15-APR-1998; 98US-0081955P.
21-APR-1998; 98US-0082568P.
21-APR-1998; 98US-0082569P.
22-APR-1998; 98US-0082700P.
22-APR-1998; 98US-0082704P.
22-APR-1998; 98US-0082804P.
23-APR-1998; 98US-0082767P.
23-APR-1998; 98US-0082796P.
27-APR-1998; 98US-0083336P.
28-APR-1998; 98US-0083322P.
29-APR-1998; 98US-0083392P.
29-APR-1998; 98US-0083495P.
29-APR-1998; 98US-0083496P.
29-APR-1998; 98US-0083499P.
29-APR-1998; 98US-0083500P.
29-APR-1998; 98US-0083545P.
29-APR-1998; 98US-0083554P.
29-APR-1998; 98US-0083558P.
29-APR-1998; 98US-0083559P.
30-APR-1998; 98US-0083742P.
05-MAY-1998; 98US-0084366P.
06-MAY-1998; 98US-0084414P.
06-MAY-1998; 98US-0084418P.
07-MAY-1998; 98US-0084598P.
07-MAY-1998; 98US-0084600P.
07-MAY-1998; 98US-0084627P.
07-MAY-1998; 98US-0084637P.
07-MAY-1998; 98US-0084639P.
07-MAY-1998; 98US-0084640P.
13-MAY-1998; 98US-0084643P.
13-MAY-1998; 98US-0085323P.
13-MAY-1998; 98US-0085338P.
15-MAY-1998; 98US-0085339P.
15-MAY-1998; 98US-0085573P.
15-MAY-1998; 98US-0085579P.
15-MAY-1998; 98US-0085580P.
15-MAY-1998; 98US-0085582P.
15-MAY-1998; 98US-0085689P.
15-MAY-1998; 98US-0085697P.
15-MAY-1998; 98US-0085700P.
15-MAY-1998; 98US-0085704P.
22-MAY-1998; 98US-0086023P.
22-MAY-1998; 98US-0086392P.
22-MAY-1998; 98US-0086414P.
22-MAY-1998; 98US-0086430P.
22-MAY-1998; 98US-0086486P.
28-MAY-1998; 98US-0087098P.
28-MAY-1998; 98US-0087106P.
28-MAY-1998; 98US-0087208P.
30-JUL-1998; 98US-0094651P.
11-SEP-1998; 98US-0100038P.
```


XX	PA	(GETH) GENENTECH INC.
XX	PI	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX	PI	WPI; 1999-551358/46.
DR	DR	N-PSDB; AA234109.
XX	XX	
XX	PT	New secreted and transmembrane polypeptides and their polynucleotides,
PT	PT	useful for treating blood coagulation disorders, cancers and cellular
PT	PT	adhesion disorders.
XX	XX	
XX	PS	Claim 12; Fig 93; 530pp; English.
XX	XX	
XX	CC	The present invention describes secreted and transmembrane polypeptides
CC	CC	and their polynucleotides. The nucleotide sequences are useful as sources
CC	CC	of probes, primers, for chromosome mapping, and for generation of
CC	CC	antisense sequences. They can also be used to create transgenic animals.
CC	CC	The proteins can be used to treat a variety of diseases and disorders,
CC	CC	depending on their function. Diseases that may be treated include blood
CC	CC	coagulation disorders, cancers and cellular adhesion disorders. They may
CC	CC	also be used to raise antibodies. AA233891 to AA234338, and AA41685 to
CC	CC	AA41774 represent polynucleotide and polypeptide sequence given in the
CC	CC	exemplification of the present invention
XX	XX	
SQ	SQ	Sequence 544 AA;
Query Match 82.6%; Score 2790.5; DB 2; Length 544;		
Best Local Similarity 84.8%; Pred. No. 1.4e-190;		
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;		
QY	1	MLPLLLSLLGGSQAMGRFIRVOESVMVEGLCISVPCSFSPROQDWTGSTPAYGYM 60
Db	1	MLPLLLSLLGGSQAMGRFIRVOESVMVEGLCISVPCSFSPROQDWTGSTPAYGYM 60
QY	61	FAVTTETTKGAVATHHQSREVMETRGFRQLTGPAGKNCGLVTRDAQMDQESQYFVRV 120
Db	61	FAVTTETTKGAVATHHQSREVMETRGFRQLTGPAGKNCGLVTRDAQMDQESQYFVRV 120
QY	121	ERGSVRYVNFMDGFFLVKTVLSFTFPRQDHTDLTCHVDFSRKGVSAQRTVRLVAVAP 180
Db	121	ERGSVRYVNFMDGFFLVKTVLSFTFPRQDHTDLTCHVDFSRKGVSAQRTVRLVAVAP 180
QY	181	RLVVISRDNTPALEPOQGNVPYLEAKQGFLLCAADSQPPATLSWLQNRVLSSS 240
Db	181	RLVVISRDNTPALEPOQGNVPYLEAKQGFLLCAADSQPPATLSWLQNRVLSSS 240
QY	241	HPWGRPRPLGLELPGVKAGDSGRYTCTAENRLGSGQQRALDLSVQYPPENLRVWVSOANRTV 300
Db	241	HPWGRPRPLGLELPGVKAGDSGRYTCTAENRLGSGQQRALDLSVQYPPENLRVWVSOANRTV 300
QY	301	LENLNGTSLPYLEGQSLCLVCTHSSPPARLSWTQRCQVLSQSPSPDPGVLELPRVQVE 360
Db	301	LENLNGTSLPYLEGQSLCLVCTHSSPPARLSWTQRCQVLSQSPSPDPGVLELPRVQVE 360
QY	361	HEGETTCHARHPLGSHVLSLSVHVSYPKLLGPCSWAEAGLHCSQSPAPSLRWL 420
Db	361	HEGETTCHARHPLGSHVLSLSVHVSYPKLLGPCSWAEAGLHCSQSPAPSLRWL 420
QY	421	GEELEGSSQDSFEVTPSSAGFWANSSLSHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
Db	387	----- 386
QY	481	DKKGLISTAFNGAFIGITALLFCLALIIIMKILPKRTQTETPRFRFHSHTILDYI 540
Db	387	-KKGLISTAFNGAFIGITALLFCLALIIIMKILPKRTQTETPRFRFHSHTILDYI 445
QY	541	NVVPTAGPLAQRNOKATNSPRTPLPGAPSPESKQKQKQYQLPSPPEPKSSQAPES 600
Db	446	NVVPTAGPLAQRNOKATNSPRTPLPGAPSPESKQKQKQYQLPSPPEPKSSQAPES 505
QY	601	QESQBELHYATLNFPGVRPEARMKPGTQADYAEVKFQ 639

Db	506	QESQBELHYATLNFPGVRPEARMKPGTQADYAEVKFQ 544
RESULT 15		
AAAB4280		
ID	AAAB4280	standard; protein; 544 AA.
XX	XX	
AC	AAAB4280;	
XX	XX	
DT	08-FEB-2001	(first entry)
XX	XX	
DE	Human PRO940 (UNQ477)	protein sequence SEQ ID NO:259.
XX	XX	
KW	Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;	
KW	expressed sequence tag; detection; cancer.	
OS	Homo sapiens.	
XX	XX	
FN	WO2000053756-A2.	
XX	XX	
PD	14-SEP-2000.	
XX	XX	
PF	18-FEB-2000; 2000WO-US004341.	
XX	XX	
PR	08-MAR-1999; 99WO-US005028.	
PR	12-MAR-1999; 99US-0123957P.	
PR	21-MAR-1999; 99US-0126773P.	
PR	21-APR-1999; 99US-0130232P.	
PR	28-APR-1999; 99US-0131445P.	
PR	14-MAY-1999; 99US-0134287P.	
PR	23-JUN-1999; 99US-0141037P.	
PR	26-JUL-1999; 99US-0145698P.	
PR	29-OCT-1999; 99US-0162506P.	
PR	30-NOV-1999; 99WO-US028313.	
PR	02-DEC-1999; 99WO-US028551.	
PR	16-DEC-1999; 99WO-US028565.	
PR	30-DEC-1999; 99WO-US030095.	
PR	30-DEC-1999; 99WO-US031243.	
PR	05-JAN-2000; 2000WO-US000219.	
PR	06-JAN-2000; 2000WO-US000277.	
PR	06-JAN-2000; 2000WO-US000376.	
XX	(GETH) GENENTECH INC.	
PA	Ashtkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;	
XX	Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen WE;	
PI	Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;	
PI	Kijavini LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;	
PI	Stewart TA, Tumas D, Williams PM, Wood WI;	
XX	WPI; 2000-611443/58.	
DR	N-PSDB; AAC78510.	
XX	Novel PRO polypeptides and polynucleotides used in detection methods, to	
PT	target bioactive molecules to specific cells, and to modulate cellular	
PT	activities.	
XX	XX	
PS	Claim 12; Fig 93; 636pp; English.	
XX	XX	
CC	AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence	
CC	tag) sequences which encode secreted or transmembrane PRO polypeptides.	
CC	The PRO polynucleotides and polypeptides have cytostatic activity. The	
CC	polynucleotides and polypeptides can be used for detecting the presence	
CC	of PRO polypeptides in samples, for linking bioactive molecules to cells	
CC	and for modulating biological activities of cells, using the polypeptides	
CC	for specific targeting. The polypeptide targeting can be used to kill the	
CC	target cells, e.g. for the treatment of cancers. The polypeptide pairs	
CC	provide specific targeting of bioactive molecules to cells. AAC78600 to	
CC	AAC78987 represent PCR primers and probes used in the isolation of the	
CC	PRO polynucleotide sequences	
XX	Sequence 544 AA;	
SQ	SQ	

Query Match 82.6%; Score 2790.5; DB 3; Length 544;
Best Local Similarity 84.8%; Pred. No. 1.4e-190;
Matches 542; Conservative 0; Mismatches 2; Indels 95; Gaps 1;

QY 1 MLLPLLLSSLLGGSQAMGRFIRVOESVWVPEGLCISVPCSFSPRODWTGTTPAYGW 60
DB 1 MLLPLLLSSLLGGSQAMGRFIRVOESVWVPEGLCISVPCSFSPRODWTGTTPAYGW 60

QY 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKNCNSLVIRDAQMDESQYFFRV 120
DB 61 FKAVTETTKGAPVATNHQREVEMSTRGRFQLTGDPKNCNSLVIRDAQMDESQYFFRV 120

QY 121 ERGSYVRYNFMNDGFTLVTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180
DB 121 ERGSYVRYNFMNDGFTLVTVLSFTPRPDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAP 180

QY 181 RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCAADSQPPATLSWVLQNEVLSSS 240
DB 181 RDLVISISRDNTPALEPQPGNVPLYEAQKGQFLRLCAADSQPPATLSWVLQNEVLSSS 240

QY 241 HPWGPRLGLPLGVVAGDSGRYTCRAENRGLSQORALDLSVOYPPENLRVWVSQANRTV 300
DB 241 HPWGPRLGLPLGVVAGDSGRYTCRAENRGLSQORALDLSVOYPPENLRVWVSQANRTV 300

QY 301 LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSPOFSDPGVLELPRVQVE 360
DB 301 LENLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTORGQVLSPOFSDPGVLELPRVQVE 360

QY 361 HEGETTCHARHPLGSHVSLSLSVHYSPKLGPSCSWEAEGLHCSQASAPSLRWL 420
DB 361 HEGETTCHARHPLGSHVSLSLSVHYSPKLGPSCSWEAEGLHCSQASAPSLRWL 420

QY 421 GEELLEGNSQDSFEVTPSSAGFWANSLSLHGLSSGLRLRCEAWNVHGAQSGSILQLP 480
DB 387 ----- 386

QY 481 DRKGLISTAFSNGAFIGITALLFLCLALIIIMKILPKERTQETPRPRFSRHSITLDYI 540
DB 387 -KKGLISTAFSNGAFIGITALLFLCLALIIIMKILPKERTQETPRPRFSRHSITLDYI 445

QY 541 NVVPTAGPLAQENQKATNSPRTPLPGAPSPESKKNQKQYQLPSPEPKSSTOAPES 600
DB 446 NVVPTAGPLAQENQKATNSPRTPLPGAPSPESKKNQKQYQLPSPEPKSSTOAPES 505

QY 601 QBSQELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 639
DB 506 QBSQELHYATLNFPGVRPRPEARMKGTQADYAEVKFQ 544

Search completed: November 5, 2004, 13:53:24
Job time : 76.3927 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2004, 13:50:17 ; Search time 74.3927 Seconds
(without alignments)
3081.324 Million cell updates/sec

Title: US-09-937-636-4

Perfect score: 3377
Sequence: 1 MLPLLLSLGGSQAMGR.....RPEARMPKGTQADYAEVKFQ 639

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 23Sep04:.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3377	100.0	639	2 AAW81023	AAW81023 Human sia
2	3377	100.0	639	3 AAY97543	AAY97543 Human obe
3	3354	99.3	639	3 AAB25580	AAB25580 CD33-like
4	3354	99.3	639	6 ADA27052	ADA27052 Human nov
5	3354	99.3	639	8 ADE85582	ADE85582 Novel hum
6	3338	98.8	697	5 AAU87087	AAU87087 Stalic ac
7	3334	98.7	697	7 ADA27153	ADA27153 Human nov
8	3334	98.7	697	7 ADD26582	ADD26582 Siglec-10
9	3334	98.7	697	8 ADI37010	ADI37010 Novel hum
10	3334	98.7	697	8 ADL82805	ADL82805 Human PRO
11	3299	97.7	622	5 AAU87075	AAU87075 Stalic ac
12	3174.5	94.0	710	7 ADD19314	ADD19314 Human sec
13	2803.5	83.0	544	5 AAU87074	AAU87074 Stalic ac
14	2790.5	82.6	544	3 AAY41724	AAY41724 Human PRO
15	2790.5	82.6	544	3 AAB44280	AAB44280 Human PRO
16	2790.5	82.6	544	4 AAU29082	AAU29082 Human PRO
17	2790.5	82.6	544	6 ABU58458	ABU58458 Human PRO
18	2790.5	82.6	544	6 ABU88006	ABU88006 Novel hum
19	2790.5	82.6	544	6 ABU84321	ABU84321 Human sec
20	2790.5	82.6	544	6 ABR61195	ABR61195 Human sec
21	2790.5	82.6	544	6 ABR65585	ABR65585 Human sec
22	2790.5	82.6	544	6 ABU95525	ABU95525 Human sec
23	2790.5	82.6	544	6 ABU82764	ABU82764 Human PRO
24	2790.5	82.6	544	6 ABU89885	ABU89885 Novel hum
25	2790.5	82.6	544	6 ABR68134	ABR68134 Human sec

26	2790.5	82.6	544	6 ABU96187	ABU96187 Novel hum
27	2790.5	82.6	544	6 ABU92618	ABU92618 Human sec
28	2790.5	82.6	544	6 ABO08695	ABO08695 Human sec
29	2790.5	82.6	544	6 ABO02747	ABO02747 Human sec
30	2790.5	82.6	544	6 ABR74901	ABR74901 Human sec
31	2790.5	82.6	544	6 ABR94663	ABR94663 Human sec
32	2790.5	82.6	544	6 ABO25226	ABO25226 Novel hum
33	2790.5	82.6	544	6 ABU85636	ABU85636 Human PRO
34	2790.5	82.6	544	6 ABU98796	ABU98796 Novel hum
35	2790.5	82.6	544	6 ABU98011	ABU98011 Novel hum
36	2790.5	82.6	544	6 ABU91717	ABU91717 Novel hum
37	2790.5	82.6	544	6 ABU72332	ABU72332 Novel hum
38	2790.5	82.6	544	6 ABU89410	ABU89410 Human PRO
39	2790.5	82.6	544	6 ABU86251	ABU86251 Human sec
40	2790.5	82.6	544	6 ABU67464	ABU67464 Human sec
41	2790.5	82.6	544	6 ABU80492	ABU80492 Human PRO
42	2790.5	82.6	544	6 ABR99410	ABR99410 Human sec
43	2790.5	82.6	544	6 ABR98800	ABR98800 Human sec
44	2790.5	82.6	544	6 ABO16323	ABO16323 Human sec
45	2790.5	82.6	544	6 ABR92223	ABR92223 Human sec

ALIGNMENTS

RESULT 1

AAW81023
ID AAW81023 standard; protein; 639 AA.

XX AAW81023;

DT 26-APR-1993 (first entry)

DE Human sialoadhesin family 4 (SAF-1) polypeptide.

XX SAF-4; sialoadhesin family; human; therapy; diagnosis; cancer;
KW inflammation; autoimmune disease; allergy; asthma; inflammation;
KW cerebellar degeneration; Alzheimer's disease; Parkinson's disease;
KW multiple sclerosis; amyotrophic lateral sclerosis; head injury;
KW septic shock; sepsis; stroke; osteoporosis; osteoarthritis;
KW ischemia reperfusion injury; cardiovascular disease; kidney disease;
KW liver disease; myocardial infarction; hypotension; hypertension; AIDS;
KW myelodysplastic syndrome; aplastic anaemia; baldness; infection.
XX Homo sapiens.

XX WO9853840-A1.

XX 03-DEC-1998.

XX 27-MAY-1998; 98WO-US010791.

XX 27-MAY-1997; 97US-0047572P.

XX (SMIX) SMITHKLINE BEECHAM CORP.

XX Kikly KK, Erickson-Miller CL;

XX WPI; 1999-080779/07.

XX N-PSDB; AAU99911.

PT New sialoadhesin family 4 polypeptides and polynucleotides - useful to treat various diseases associated with SAF-4 expression.

XX Claim 1; Page 31; 48pp; English.

XX This is the amino acid sequence of new human sialoadhesin family 4 (SAF-4), as deduced from the nucleotide sequence of an isolated cDNA clone (see AAU99911). SAF-4 polynucleotides and polypeptides, and methods for producing such polypeptides in transformed host cells using recombinant techniques are disclosed. SAF-4, its agonists and antagonists, and nucleic acid molecules that enhance or inhibit SAF-4 expression, may be used to treat patients in need of enhancement or inhibition of SAF-4

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expression or activity. Conditions that may benefit from such treatment include cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, head injury damage and other neurological disorders, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischemia reperfusion injury, cardiovascular disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes and other hematologic abnormalities, aplastic anaemia, male baldness pattern and bacterial, protozoal, fungal and viral infections related to SAF-4 polypeptide activity. Methods of identifying agonists, antagonists/inhibitors are also provided, as well as diagnostic assays for detecting diseases associated with inappropriate SAF-4 activity or levels

XX Sequence 639 AA;

Query Match: 100.0%; Score 3377; DB 2; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 Db 1 MLLPILLSLLGSGQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 Db 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDPSFKGVSAGRTVRLRVAYAP 180
 Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDPSFKGVSAGRTVRLRVAYAP 180
 QY 181 RDLVISIRSDNTPALPQPCGNVPYLEAKGQFLRLCAADSOPTATLSWLNQNRVLSS 240
 Db 181 RDLVISIRSDNTPALPQPCGNVPYLEAKGQFLRLCAADSOPTATLSWLNQNRVLSS 240
 QY 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVSOANRTV 300
 Db 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVSOANRTV 300
 QY 301 LENLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSFQSDSPGVLELPRVQVE 360
 Db 301 LENLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSFQSDSPGVLELPRVQVE 360
 QY 361 HEGEFTCHARHPLGSHVSLSVHSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420
 Db 361 HEGEFTCHARHPLGSHVSLSVHSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420
 QY 421 GBELLEGNSSQDSFEVTPSAGPWANSSLSHGGLSGRLRCEAWNVHGAQSGSILQLP 480
 Db 421 GBELLEGNSSQDSFEVTPSAGPWANSSLSHGGLSGRLRCEAWNVHGAQSGSILQLP 480
 QY 481 DKKGLISTAFNSGAFILGIGITALLFLCLALIMKILPKRRTOTETPRPFSRHSITLDYI 540
 Db 481 DKKGLISTAFNSGAFILGIGITALLFLCLALIMKILPKRRTOTETPRPFSRHSITLDYI 540
 QY 541 NVVPTAGPLAQRNQKATNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSSSQAPES 600
 Db 541 NVVPTAGPLAQRNQKATNSPRTPLPGAPSPESKKNQKQYQLPSPFPKSSSQAPES 600
 QY 601 QESQBELHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ 639
 Db 601 QESQBELHYATLNFPGVRPRPBARMPKGTQADYAEVKFQ 639

RESULT 2

AA97543

ID AA97543 standard; protein; 639 AA.

XX

AC AA97543;

XX

12-FEB-2001 (first entry)

XX Human obesity protein binding protein-2 homologue #2.
 DE Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity;
 XX obesity-related disorder; therapy.
 KW Homo sapiens.
 OS WC200059942-A2.
 FN 12-OCT-2000.
 PD 22-MAR-2000; 2000WO-US006692.
 PP 02-APR-1999; 99US-0127667P.
 PR (ELIL) LILLY & CO ELI.
 XX Su EW, Wei J;
 PI WPI; 2000-664992/64.
 XX N-PSDB; NAA37848.
 DR New human obesity protein binding protein-2 homologue nucleic acids,
 PT polynucleotides and polypeptides useful for producing medicament for
 PT treating obesity and/or obesity-related disorders.
 XX Claim 9; Page 89-91; 92pp; English.

XX This sequence is a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro.
 CC Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides

Sequence 639 AA;

Query Match: 100.0%; Score 3377; DB 3; Length 639;
 Best Local Similarity 100.0%; Pred. No. 2.3e-232;
 Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLLPILLSLLGSGQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 Db 1 MLLPILLSLLGSGQAMDGFWIRVQESVMVPEGLCISVPCSFSPRODWTGSTPAYGW 60
 QY 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 Db 61 FKAVTETTKGAPVATNHQSEVEMSTRGRFQLTGDPKAGNCSLVIRDAQMDESQYFFRV 120
 QY 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDPSFKGVSAGRTVRLRVAYAP 180
 Db 121 ERGSYVRYNFMNDGFFLKVTLSFTPRPDHNTDLTCHVDPSFKGVSAGRTVRLRVAYAP 180
 QY 181 RDLVISIRSDNTPALPQPCGNVPYLEAKGQFLRLCAADSOPTATLSWLNQNRVLSS 240
 Db 181 RDLVISIRSDNTPALPQPCGNVPYLEAKGQFLRLCAADSOPTATLSWLNQNRVLSS 240
 QY 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVSOANRTV 300
 Db 241 HPWGPRPLGLELPGVKGAGSGRYTCRAENRLGSGQALDLSVQYPPENLRVMVSOANRTV 300
 QY 301 LENLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSFQSDSPGVLELPRVQVE 360
 Db 301 LENLNGTSLPVLEGQSLCLVCTHSSPPARLSWTORGQVLSFQSDSPGVLELPRVQVE 360
 QY 361 HEGEFTCHARHPLGSHVSLSVHSPKLLGPSCSWEAEGHLCSSQASAPSLRWL 420

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